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OM protein - protein search, using sw model

Run on: July 2, 2003, 16:49:50 ; Search time 15.5397 Seconds  
(without alignments)  
799.016 Million cell updates/sec

Title: US-09-857-583-4

Perfect score: 2283

Sequence: 1 MKSRQALSPLQMEQTDV.....LRYLAVFARMAEKQPAKGL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents\_AA:\*
- 1: /cgn2.6/ptodata/1/1aa/5A\_COMB.pep.\*
  - 2: /cgn2.6/ptodata/1/1aa/5B\_COMB.pep.\*
  - 3: /cgn2.6/ptodata/1/1aa/6A\_COMB.pep.\*
  - 4: /cgn2.6/ptodata/1/1aa/6B\_COMB.pep.\*
  - 5: /cgn2.6/ptodata/1/1aa/PTUS\_COMB.pep.\*
  - 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	631	27.6	457	2	US-08-834-655-2	Sequence 2, Appl1
2	631	27.6	457	3	US-08-834-033A-2	Sequence 2, Appl1
3	631	27.6	457	4	US-09-363-574-2	Sequence 2, Appl1
4	631	27.6	457	4	US-09-363-526-2	Sequence 2, Appl1
5	631	27.6	457	4	US-09-330-235-18	Sequence 18, Appl1
6	631	27.6	458	4	US-09-439-261-10	Sequence 10, Appl1
7	631	27.6	458	4	US-09-439-261-44	Sequence 44, Appl1
8	631	27.6	458	4	US-09-227-613-11	Sequence 11, Appl1
9	631	27.6	458	4	US-09-227-613-41	Sequence 41, Appl1
10	622	27.2	457	2	US-08-833-610-4	Sequence 4, Appl1
11	622	27.2	457	3	US-08-834-033A-14	Sequence 14, Appl1
12	565	24.7	355	2	US-08-834-655-5	Sequence 5, Appl1
13	565	24.7	355	3	US-08-834-033A-6	Sequence 6, Appl1
14	565	24.7	355	4	US-09-363-574-5	Sequence 5, Appl1
15	565	24.7	355	4	US-09-363-526-5	Sequence 5, Appl1
16	524.5	23.0	323	4	US-09-439-261-17	Sequence 17, Appl1
17	524.5	23.0	323	4	US-09-227-613-17	Sequence 17, Appl1
18	461	20.2	452	4	US-08-934-254-27	Sequence 27, Appl1
19	433.5	19.0	448	1	US-08-366-779-5	Sequence 5, Appl1
20	433.5	19.0	448	1	US-08-789-936-5	Sequence 5, Appl1
21	433.5	19.0	448	4	US-08-934-254-5	Sequence 5, Appl1
22	430.5	18.9	446	2	US-08-833-610-5	Sequence 5, Appl1
23	430.5	18.9	446	3	US-08-834-033A-15	Sequence 15, Appl1
24	426	18.7	432	4	US-09-439-261-9	Sequence 9, Appl1
25	426	18.7	432	4	US-09-227-613-9	Sequence 9, Appl1
26	426	18.7	465	4	US-09-439-261-40	Sequence 40, Appl1
27	426	18.7	465	4	US-09-227-613-38	Sequence 38, Appl1

28	416	18.2	444	4	US-09-439-261-11	Sequence 11, Appl1
29	416	18.2	444	4	US-09-227-613-12	Sequence 12, Appl1
30	416	18.2	445	4	US-09-439-261-39	Sequence 39, Appl1
31	416	18.2	445	4	US-09-439-261-45	Sequence 45, Appl1
32	402.5	17.6	444	4	US-09-439-261-43	Sequence 43, Appl1
33	402.5	17.6	444	4	US-09-227-613-42	Sequence 42, Appl1
34	312.5	13.7	356	4	US-09-439-261-19	Sequence 19, Appl1
35	312.5	13.7	356	4	US-09-227-613-18	Sequence 18, Appl1
36	305	13.4	287	4	US-09-439-261-13	Sequence 13, Appl1
37	305	13.4	287	4	US-09-227-613-14	Sequence 14, Appl1
38	305	13.4	288	4	US-09-439-261-16	Sequence 16, Appl1
39	305	13.4	288	4	US-09-439-261-18	Sequence 18, Appl1
40	305	13.4	288	4	US-09-227-613-15	Sequence 15, Appl1
41	305	13.4	288	4	US-08-834-655-7	Sequence 7, Appl1
42	277.5	12.2	252	2	US-08-834-033A-8	Sequence 8, Appl1
43	277.5	12.2	252	3	US-09-363-574-7	Sequence 7, Appl1
44	277.5	12.2	252	4	US-09-363-526-7	Sequence 7, Appl1
45	277.5	12.2	252	4		

## ALIGNMENTS

### RESULT 1

US-08-834-655-2  
Sequence 2, Application US/08834655

Patent No. 5968809

GENERAL INFORMATION:

APPLICANT: KNUZON, DEBORAH

APPLICANT: MURKERT, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATING APPLICATION NUMBER: US/08/834,655

FILING DATE: 11-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.124.0005

TELEPHONE: (650) 328-4400

TELEFAX: (650) 328-4477

TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-655-2

Query Match 27.6%; Score 631; DB 2; Length 457;

Best Local Similarity 33.0%; Pred. No. 7.6e-66;

Matches 150; Conservative 76; Mismatches 173; Indels 56; Caps 11;

Qy	2	KSRQALSPQLM--EOTYDVSAVWNFHPGGAEIENYQGRDATDAFVMHFQEAFLDKL 59
Db	23	EGKDAEAPFLMIIDKNKYIDVREFVDPHGGG-VILTHVGKDGTVDTFTFHPAAAWETL- 80
Qy	60	RMPKINPFFELPPQAAVNEAQEDF-----RKLREELIATGFDASPLWYSKYKIST 110
Db	81	-----ANFYV--GDIDESDRDITKNDFFAAEVYKRLTFLQSLGYDSSKAYIAFKVFN 131
Qy	111	LGGLVGYFLMVQYOM-----YFIGAVLLGMHYQOMGWSLHSDICHQHQTFFKNRNWNVL 165
Db	132	LCIINGLSTVIAVAKGQSTLANVLSAALLGLFWQCGWLADHFLHQVQDFRFGDLFGA 191
Qy	166	VFGNGLGQSVTCWKDRHNAHSTNYQGHDPDIDNPLPAWSEDDVTRASPI----- 218
Db	192	FLGVCVCGFSSWWKDKHNTHHAAPNVHGEDPIDHTPLLTWSEHALEWFSVDPDEELTR 251
Qy	219	--SRKLQFOQYFELVACILHRFTWCFCQVLTVRSLKDRDNQFYRSQYKK-----EATG 270
Db	252	MWSRFVNLQNTWFYFIPILSPARLSKWLQSLFVLP---NGOAHKPSGARVPISLVEQLS 307
Qy	271	LALHWTILKALFHLFPMFSPILTSLLVFFVSELVGGEGIAIVFNMNHYPLEKIGDPVWDGHG 330
Db	308	LAMHWTYLATMFLFIKDPVNMNLYFVLSQVCGNLLAIVFSLNHGMPVISEKEAVDMD 367
Qy	331	FSVQGIETHMTNIRGIITDWFPGGLNYQIEHHLWPTLPRHNLTAVSVOEOLCKOHNLPY 390
Db	368	FFTKQIITGRDVHGPLFANWTFGGLNYQIEHHLFPMRPNRPNFSKTOPAVETLCKYVRY 427
Qy	391	RNPLPHGGLVLLRYLAVFARMAEKQPA-----GKA 421
Db	428	HTTGMIIGTA-----EVFSLNEYSKAAKMGKA 456

## RESULT 2

US-08-834-033A-2  
: Sequence 2, Application US/08834033A  
: Patent No. 6075183  
: GENERAL INFORMATION:  
: APPLICANT: KNUTZON, DEBORAH  
: APPLICANT: MUKERJI, PRADIP  
: APPLICANT: HUANG, YUNG-SHENG  
: APPLICANT: THURMOND, JENNIFER  
: APPLICANT: CHAUDHARY, SUNITA  
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
: TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
: NUMBER OF SEQUENCES: 26  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.  
: STREET: 2001 FERRY BUILDING  
: CITY: SAN FRANCISCO  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94111  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: WORDPERFECT 5.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/834,033A  
: FILING DATE: 11-APR-1997  
: CLASSIFICATION: 800  
: ATTORNEY/AGENT INFORMATION:  
: NAME: WARD, MICHAEL R.  
: REGISTRATION NUMBER: 38,651  
: REFERENCE/DOCKET NUMBER: CGAB-300.USA  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 433-4150  
: TELEFAX: (415) 433-8716  
: TELEX: N/A  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 457 amino acids

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; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-2

Query Match 27.6%; Score 631; DB 4; Length 457;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPQLM--EQTVDYSAWVNFHPGAGAEIENYQGRDATDAFVMVHFQEAFLK 59
Db 23 EGKKADEAPFLMIIDNKVDYREFVDPHGGG-VILTHVGKDGTDVDFTHPEAAWETL- 80
QY 60 RMPKINPSPFLPQAAVNEAQEDF-----RKLREELIATCMFDPASPLWYSYKISTT 110
Db 81 -----ANFVY---GDIDESDRDIKNDFFAEVRKLTFLQSLGYDSSKAYAFKVSFN 131
QY 111 LGLGVLGYFLMVQYQM-----YFTGAVLLGMHYQOMGLSHDICHHTQTFKNNMNNLVGL 165
Db 132 LCITWGLSTVIVAKWGQTSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFWGDLEGA 191
QY 166 VFCNGLOGSVTCWKDRHNAHSHATNVQGHDPDIDNLPPLANSEDDVTRASPI----- 218
Db 192 FLGGVCGGFSSSWKKDKHNTTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVPDEBLTR 251
QY 219 --SRKLQFOQYVFLVICILLRFTWCFCQVLTVRSLKDRDNQFVRSQYKK-----EAIG 270
Db 252 MNSRFVNLQNTWFFPILSFARLSWCLOSILFVLP-----NGQAHKPGCARVPISLVEQLS 307
QY 271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGFGIAIVVFMNHYPLEKIGDPVWDG 330
Db 308 LAMHWTWYLATMFLFKIDPVMNLVFLVSAQVCGNLLAIVFSLNHNHGMPIVSKREEAVDMD 367
QY 331 FSVGQIHTETMNIIRGIITDHFQGLNLYQIEHLLWPTLPRNLTAVSYQVQLCKHNL 390
Db 368 FTKQIITGRDVHPGLFANFTGGLNLYQIEHLLFSPMRHNFSKIOPAVETLCKKNVRY 427
QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
Db 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 4
US-09-363-526-2
; Sequence 2, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SONITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-526-2

Query Match 27.6%; Score 631; DB 4; Length 457;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPQLM--EQTVDYSAWVNFHPGAGAEIENYQGRDATDAFVMVHFQEAFLK 59
Db 23 EGKKADEAPFLMIIDNKVDYREFVDPHGGG-VILTHVGKDGTDVDFTHPEAAWETL- 80
QY 60 RMPKINPSPFLPQAAVNEAQEDF-----RKLREELIATCMFDPASPLWYSYKISTT 110
Db 81 -----ANFVY---GDIDESDRDIKNDFFAEVRKLTFLQSLGYDSSKAYAFKVSFN 131
QY 111 LGLGVLGYFLMVQYQM-----YFTGAVLLGMHYQOMGLSHDICHHTQTFKNNMNNLVGL 165
Db 132 LCITWGLSTVIVAKWGQTSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFWGDLEGA 191
QY 166 VFCNGLOGSVTCWKDRHNAHSHATNVQGHDPDIDNLPPLANSEDDVTRASPI----- 218
Db 192 FLGGVCGGFSSSWKKDKHNTTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVPDEBLTR 251
QY 219 --SRKLQFOQYVFLVICILLRFTWCFCQVLTVRSLKDRDNQFVRSQYKK-----EAIG 270
Db 252 MNSRFVNLQNTWFFPILSFARLSWCLOSILFVLP-----NGQAHKPGCARVPISLVEQLS 307
QY 271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGFGIAIVVFMNHYPLEKIGDPVWDG 330
Db 308 LAMHWTWYLATMFLFKIDPVMNLVFLVSAQVCGNLLAIVFSLNHNHGMPIVSKREEAVDMD 367
QY 331 FSVGQIHTETMNIIRGIITDHFQGLNLYQIEHLLWPTLPRNLTAVSYQVQLCKHNL 390
Db 368 FTKQIITGRDVHPGLFANFTGGLNLYQIEHLLFSPMRHNFSKIOPAVETLCKKNVRY 427
QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
Db 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 5
US-09-330-235-18
; Sequence 18, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO 156,00DS
; CURRENT APPLICATION NUMBER: US/09/330,235
; CURRENT FILING DATE: 1999-06-10
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Query Match 27.6%; Score 631; DB 4; Length 458;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPLQIM--EQTYDVSANVNFHPGGAIEIENVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIG 270
DB 23 EGKDAEAPFLMIIDNKYIDVREFVDPHPGGS-VILTHVGKDGTDVDFTEHPEAAWETL- 80

QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKISTT 110
DB 81 -----ANFYV---GDIDESORDIKNDFFAAEVRKRLTLFOSLGYDSSKAYIAFKVSFN 131

QY 111 LGLVGLGYFLMVQYQM-----YFIGAVLLGMHYQOMGWSLSDICHCHOTFKNRNNNLVGL 165
DB 132 LCINGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLADFLHHQVFOQDFRFGDLFGA 191

QY 166 VFGNGLQGSVTCWKDRNNAHSAFNVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIG 270
DB 192 FLGGVCOGFSWSSWKKDKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDVDELT 251

QY 219 --SRKLIQOQYFYFLVICILLRFIWCFCQVLTVRSKDRDNQFYSQYKK-----EAIG 270
DB 252 MWSRPMVLNQTWFYFPILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307

QY 271 LALHWTALKALFHLFMPSTLTSLLVFFVSELVGGGIAIVVFMNHYPLEKIGDPVWDGHC 330
DB 308 LAMHTWYLATMFLFKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNHMPVISKEEAVDMD 367

QY 331 FSVGQIHETMIRRIITDWFPGGLNYQIEHHLWPTLPRHNLTAVSQYQVCOCKHNL 390
DB 368 FFTKQIITGRDVHPCGFANWFTGGLNYQIEHHLFSPMPRHNSKIQPAVETLCKKYNRY 427

QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMIETA-----EVFSRLNEYSKAASKMGKA 456

RESULT 8
US-09-227-613-11
; Sequence 11, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 458 is unknown or other.
US-09-227-613-11

Query Match 27.6%; Score 631; DB 4; Length 458;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPLQIM--EQTYDVSANVNFHPGGAIEIENVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIG 270
DB 23 EGKDAEAPFLMIIDNKYIDVREFVDPHPGGS-VILTHVGKDGTDVDFTEHPEAAWETL- 80

QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKISTT 110
DB 81 -----ANFYV---GDIDESORDIKNDFFAAEVRKRLTLFOSLGYDSSKAYIAFKVSFN 131

QY 111 LGLVGLGYFLMVQYQM-----YFIGAVLLGMHYQOMGWSLSDICHCHOTFKNRNNNLVGL 165
DB 132 LCINGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLADFLHHQVFOQDFRFGDLFGA 191

QY 166 VFGNGLQGSVTCWKDRNNAHSAFNVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIG 270
DB 192 FLGGVCOGFSWSSWKKDKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDVDELT 251

QY 219 --SRKLIQOQYFYFLVICILLRFIWCFCQVLTVRSKDRDNQFYSQYKK-----EAIG 270
DB 252 MWSRPMVLNQTWFYFPILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307

QY 271 LALHWTALKALFHLFMPSTLTSLLVFFVSELVGGGIAIVVFMNHYPLEKIGDPVWDGHC 330
DB 308 LAMHTWYLATMFLFKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNHMPVISKEEAVDMD 367

QY 331 FSVGQIHETMIRRIITDWFPGGLNYQIEHHLWPTLPRHNLTAVSQYQVCOCKHNL 390
DB 368 FFTKQIITGRDVHPCGFANWFTGGLNYQIEHHLFSPMPRHNSKIQPAVETLCKKYNRY 427

QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMIETA-----EVFSRLNEYSKAASKMGKA 456

RESULT 8
US-09-227-613-11
; Sequence 11, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Xaa at position 458 is unknown or other.
US-09-227-613-11

Query Match 27.6%; Score 631; DB 4; Length 458;
Best Local Similarity 33.0%; Pred. No. 7.6e-66;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPLQIM--EQTYDVSANVNFHPGGAIEIENVOGHDPIDNLPPLAWSEDDVTRASPI-----EAIG 270
DB 23 EGKDAEAPFLMIIDNKYIDVREFVDPHPGGS-VILTHVGKDGTDVDFTEHPEAAWETL- 80

QY 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKISTT 110
DB 81 -----ANFYV---GDIDESORDIKNDFFAAEVRKRLTLFOSLGYDSSKAYIAFKVSFN 131
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QY 271 LALHWTILKALFLHFFMPSILTSLLVFFVSELVGGGIAIVVEMNHYPLEKIGDPVWDG 330  
 DB 308 LAMHWTYLATMFLFKDPVNMVLYFLVSAVCGNLLAIVFSLNHNHGMPIVSEAEVMD 367  
 QY 331 FSVGQIHTMNIIRGIITDFFGGLNLYQIEHLLWPTLPRHNLTAIVSYQVBLCKQKHNLPY 390  
 DB 368 FFTKQIITGRDVHPLGFANFTGGLNLYQIEHLLWPTLPRHNLTAIVSYQVBLCKQKHNLPY 427  
 QY 391 RNPPLHGLVILLRYLAVFARMAEKOPA-----GKA 421  
 DB 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 10

US-08-833-610-4  
 ; Sequence 4, Application US/08833610  
 ; Patent No. 5972664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KNUTZON, DEBORAH  
 ; APPLICANT: MURKERJI, PRADIP  
 ; APPLICANT: HUANG, YUNG-SHENG  
 ; APPLICANT: THURMOND, JENNIFER  
 ; APPLICANT: CHAUDHARY, SUNITA  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
 ; STREET: 260 SHERIDAN AVE, P.O. BOX 60039  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94306

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/08/833,610  
 ; FILING DATE: 11-APR-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: RAE-VENTER, BARBARA  
 ; REGISTRATION NUMBER: 32,750  
 ; REFERENCE/DOCKET NUMBER: CGNE.123.000S  
 ; TELEPHONE: (650)328-4400  
 ; TELEFAX: (650)328-4477  
 ; TELEX: N/A  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 457 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-833-610-4

Query Match 27.2%; Score 622; DB 2; Length 457;  
 Best Local Similarity 32.7%; Pred. No. 8.8e-65;  
 Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;  
 QY 2 KSRQALSPQLM--EQTYSVSAWNPHPGGAELIENYQGRDATDAPVMWHFOAFK 59  
 DB 23 EGKDAEAPFLMIDNKVDYREFVDPHGGG-VILTHVGKGDVDFTEHPEAAWETL- 80  
 QY 60 RMPKINPSFELPQAAVNEAQEDF-----RKLREELIATGMFDPASLWYSKISIT 110  
 DB 81 -----ANFYV---GDIDESDRDIKNDFFAAEVKRLTFLQSLGYDSSKAYAFKVSFN 131  
 QY 111 LGLGVLYGLVWQYQM-----YFIGAVLLGMHYQOMGLSHDICHCHOTFKNRNWNLVGL 165

DB 132 LCITWGLSTIVAKWGQSTLTANLVLSAALLGLFWQCCGLAHDFLHHQVQDFRWGDLFGA 191  
 QY 166 VFGNGLOGFSVTKWDRHNAHSATNTVQGHDPDIDNLPPLAWSDDVTRASPI----- 218  
 DB 192 FLGGVCGQFSSWKKDKHNTHAAPNVHVEDPDIDTHTPLTWSHHALEMESDVPDEELTR 251  
 QY 219 --SRKLIQFOQYVFLVICILLRFTWCFCVLTVRSLKDRDNQFYRSQYKK-----EAIG 270  
 DB 252 MWSRFVNLNQTWTFYFPLSFAKLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEOLS 307  
 QY 271 LALHWTILKALFLHFFMPSILTSLLVFFVSELVGGGIAIVVEMNHYPLEKIGDPVWDG 330  
 DB 308 LAMHWTYLATMFLFKDPVNMVLYFLVSAVCGNLLAIVFSLNHNHGMPIVSEAEVMD 367  
 QY 331 FSVGQIHTMNIIRGIITDFFGGLNLYQIEHLLWPTLPRHNLTAIVSYQVBLCKQKHNLPY 390  
 DB 368 FFTKQIITGRDVHPLGFANFTGGLNLYQIEHLLWPTLPRHNLTAIVSYQVBLCKQKHNLPY 427  
 QY 391 RNPPLHGLVILLRYLAVFARMAEKOPA-----GKA 421  
 DB 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 11

US-08-834-033A-14  
 ; Sequence 14, Application US/08834033A  
 ; Patent No. 6075183  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KNUTZON, DEBORAH  
 ; APPLICANT: MURKERJI, PRADIP  
 ; APPLICANT: HUANG, YUNG-SHENG  
 ; APPLICANT: THURMOND, JENNIFER  
 ; APPLICANT: CHAUDHARY, SUNITA  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.  
 ; STREET: 2001 FERRY BUILDING  
 ; CITY: SAN FRANCISCO  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WORDPERFECT 5.1  
 ; CURRENT APPLICATION DATA: US/08/834,033A  
 ; FILING DATE: 11-APR-1997  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WARD, MICHAEL R.  
 ; REGISTRATION NUMBER: 38,651  
 ; REFERENCE/DOCKET NUMBER: CGAB-300.USA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 433-4150  
 ; TELEFAX: (415) 433-8716  
 ; TELEX: N/A  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 457 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-834-033A-14

Query Match 27.2%; Score 622; DB 3; Length 457;  
 Best Local Similarity 32.7%; Pred. No. 8.8e-65;  
 Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;





```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-526-5

Query Match      24.7%; Score 565; DB 4; Length 355;
Best Local Similarity 34.9%; Pred. No. 3.3e-58;
Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

Qy 82 DFRKLRLELIATGMFDASPLMYSKISTTIGLGVFLWVQYQ-----YFIGAVLLGM 136
Db 1 EVKRLTLFQSLGYDSKAYAFKVSFNICIGWLSIVIVAKWGOTSTLANVLSAALLGL 60

Qy 137 HYQMGWNLSDHCHQTFKNRNWNLVGLVFGNGLQGFSVTCWKDRHNAHSAATNVQGH 196
Db 61 FWOQCGWLADFLHHQVDFDRFGDLFGAFLGGVCGQGFSSSWKDKHNTHTAAPNVHGED 120

Qy 197 PDIDNLPPLAWSEDDVTRASPI-----SRKLIQOQYFLVICILLRPIWCFQCVL 247
Db 121 PDIDTHPLLTWSEHALEHFSVDPDELTRMWSRFMVLNQTWFFPILSFARLSWCLQSIL 180

Qy 248 TVRSLKDRDNQFYRSQYKK-----EAGLALHWTALKALFHLFFMPSTLTSLLVFFVSEL 301
Db 181 FVLP-----NGAHFPGSGARVPISLVEQLSLAHHTWYLATWFLFKDPVNMVFLVSQA 236

Qy 302 VGGEGIAIVVPMNHYPLEKIGDPVWDGHGFSVGQIHTETMNIIRGIITDWFEGGLNYQIEH 361
Db 237 VCGNLLAIVFSLNHGMPVISKEEAVDMDFTKIITGRDVHPGLFANWFTGGLNYQIEH 296

Qy 362 HLWPTLPRHNLTAISYQVEQLCQKHNLPYRNPLPHEGLVILLRYLAVFARMAEKQPA--- 418
Db 297 HLFPSMPRHPNFSKIOPAVETLCKKYNRYHTTGMEGTA-----EVSRLNEYSKAASK 350

Qy 419 -GKA 421
Db 351 MGKA 354
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Search completed: July 2, 2003, 19:28:45  
Job time : 17.5397 secs



Db 81 -----ANFVV---GDIKNDKNDFAAEVRKRLTFLQSLGYDDSSKAYFAKVSFN 131  
QY 111 LGLVGLGYLWVQYQ-----YFIVGAVLLGMHYQMGWLSHDICHQHTFKNRNNWNLVGL 165  
Db 132 LCITWGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFWGLFGA 191  
QY 166 VFGNGLQGSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPI----- 218  
Db 192 FLGGVCGGSSSSWKDKHNTHAAPNVHGEDPDIDHPLLTWSEHALEMFSVDPDELT 251  
QY 219 --SRKLIQFOOYFVLICILLRIFWCFOCVLTVRSKDRDNQFYRSQYK-----BAIG 270  
Db 252 MNSRFVNLQNTWFFILSFARLSWCLQSILFVLP-----NGAHKPSGARVPISLVEQLS 307  
QY 271 LAHWTLKALFLHFFMPSILTSLLVFFVSELVCGFGIAIVVFNHNPYLEKIGDPVWDGHC 330  
Db 308 LAHWTWYLATWFLFKIDPVNMLVFLVSOAVCGNLLAIVFSLNHNMPVISEEAVDMD 367  
QY 331 FSVGQIHTWNTIRRGITDWFGLGNYQIEHHLWPTLPRHNLTAVSQVQECOLCKHNL 390  
Db 368 FTKQIITGRDHPGLFANWFTGGLNYQIEHHLFPPMHRNFNSKIQAIVETLCKKNVRY 427  
QY 391 RNPPLHEGLVILLRYLAVFARMAEKOPA-----GKA 421  
Db 428 HTTGMIEGTA-----EVSRLNEVSKAASKMGKA 456

## RESULT 2

US-10-191-513A-41  
; Sequence 41, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295-US-D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (458)...(458)  
; OTHER INFORMATION: xaa - Unknown or other at position 458  
US-10-191-513A-41

Query Match 27.6%; Score 631; DB 9; Length 458;  
Best Local Similarity 33.0%; Pred. No. 3.9e-57;  
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;  
QY 2 KSKROALSPQLM--EQTYDVSANVFNHFGGAEIENYQGRDATDAFVMMHFOEADFKL 59  
Db 23 EGKDAEAPPLMIIDNKVDYREFVDPHGG--VILTHVCKDGTDFDTHPEAAWETL- 80  
QY 60 RPKINPSFELPQAAVNEAQEDF-----RKLREELIATGMFDPASLWTSYKISTT 110  
Db 81 -----ANFVV---GDIKNDKNDFAAEVRKRLTFLQSLGYDDSSKAYFAKVSFN 131  
QY 111 LGLVGLGYLWVQYQ-----YFIVGAVLLGMHYQMGWLSHDICHQHTFKNRNNWNLVGL 165

Db 132 LCITWGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFWGLFGA 191  
QY 166 VFGNGLQGSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPI----- 218  
Db 192 FLGGVCGGSSSSWKDKHNTHAAPNVHGEDPDIDHPLLTWSEHALEMFSVDPDELT 251  
QY 219 --SRKLIQFOOYFVLICILLRIFWCFOCVLTVRSKDRDNQFYRSQYK-----BAIG 270  
Db 252 MNSRFVNLQNTWFFILSFARLSWCLQSILFVLP-----NGAHKPSGARVPISLVEQLS 307  
QY 271 LAHWTLKALFLHFFMPSILTSLLVFFVSELVCGFGIAIVVFNHNPYLEKIGDPVWDGHC 330  
Db 308 LAHWTWYLATWFLFKIDPVNMLVFLVSOAVCGNLLAIVFSLNHNMPVISEEAVDMD 367  
QY 331 FSVGQIHTWNTIRRGITDWFGLGNYQIEHHLWPTLPRHNLTAVSQVQECOLCKHNL 390  
Db 368 FTKQIITGRDHPGLFANWFTGGLNYQIEHHLFPPMHRNFNSKIQAIVETLCKKNVRY 427  
QY 391 RNPPLHEGLVILLRYLAVFARMAEKOPA-----GKA 421  
Db 428 HTTGMIEGTA-----EVSRLNEVSKAASKMGKA 456

## RESULT 3

US-09-967-477B-8  
; Sequence 8, Application US/09967477B  
; Patent No. US20020156254A1  
; GENERAL INFORMATION:  
; APPLICANT: Xisao Qiu  
; APPLICANT: Haiping Hong  
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL  
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: BNZ-001  
; CURRENT APPLICATION NUMBER: US/09/967,477B  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/236,303  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/297,562  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Thraustochytrium sp.  
US-09-967-477B-8

Query Match 26.3%; Score 601; DB 9; Length 459;  
Best Local Similarity 31.6%; Pred. No. 5.2e-54;  
Matches 142; Conservative 80; Mismatches 167; Indels 60; Gaps 12;  
QY 2 KSKROALSP-----LQLMEOQTYDVSANVFNHFGGAEIENYQGRDATDAFVMMHFOEADFK 57  
Db 15 KEIREHATPATATWIVIHKKVYDISKW--DSHPGGS--VMLTQAGEDATDAFAVHFPSALKL 72  
QY 58 LKRW-----PKINPSFELPQAAVNEAQEDFRLREELIATGMFDPASPL 101  
Db 73 LEQFYVGDVDSETSKEIETEGEPASDE--ERARRERINEFIASRYRLRVKVKMGGLYDASAL 130  
QY 102 WYSYKISTTLGLGLVGLY---FLMVOYOMYFIVGAVLLGMHYQMGWLSHDICHQHTFKNRN 158  
Db 131 YYAWKLVTSTGIAVLSNAICFFNFNSFAMVAVGIMGLFYQOSGLAHDFLHNQVCENT 190  
QY 159 WNNLVGLVFGNGLQGSVTCWKDRHNAHSATNVQ-----HDPIDNLPPLAWSEDD 211  
Db 191 LGNLIGLVGNAGWGSFQWQKNHNLHVAVNLHSAKDEGFIGDPDIDTTPLLAWSKEM 250  
QY 212 VTRA--SPIRKLIOFOOYFVLICILLRIFWCFOCVLTVRSKDRDNQFYRSQYK--- 266  
Db 251 ARKAFESAHGFFFTIRNOAFLYFPLLLARLSWLAQSFYVFT-----EFSFGIDFKVEF 304  
QY 267 --EAILGALHWLTKALFLHFFMPSILTSLLVFFVSELVCGFGIAIVVFNH---YPL 318

Db 305 DGPEKAGLVHYIWLQAIPTFCNMSLPEGVAYFLMQASCGLLLALVFSIGHNGMSYTER 364  
Qy 319 EKIGDPVWDGHSVQGIHETMNRIRGITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQY 378  
Db 365 ETKPD-----FQQLQVTTTRNRASVFMDFGTGGLNYQIDHHLFPLVPRHNLPKVNL 417  
Qy 379 VEOLCOKHNLPRNPLPHEGLVILLRYLA 407  
Db 418 IKSCKEDFDIFHETGFWEGYEVVDHLA 446

## RESULT 4

US-10-191-513A-17  
; Sequence 17, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (323)...(323)  
; OTHER INFORMATION: Xaa - Unknown or other at position 323  
US-10-191-513A-17

Query Match 23.0%; Score 524.5; DB 9; Length 323;  
Best Local Similarity 36.9%; Pred. No. 3e-46;  
Matches 115; Conservative 45; Mismatches 123; Indels 29; Gaps 5;  
Qy 129 IGAVLLGMHYQMGWLSHDICHQTEKRNWNNLVGLVFGNGLOGESVTCCKDRNNAHS 188  
Db 20 LSAALLGFWQCCGLAHLDFLHVQFQDRFGWDLFGAFLGVCGGFSSSWWKDKHNTHA 79  
Qy 189 ATNVQGHDPDIDNPLPLAWSDDYTRASPI-----SRKLQFOQYYFLVICILRF 239  
Db 80 APNVHGEDPDIDTHTPLTWSEHALEMFSVDEELTRWRSFVNLQWTFYFPLSPARL 139  
Qy 240 IKFCQCVLTVRSKDRNQFVRSYKK-----BAIGLALHTWLKALFLHFFMPSILTSL 293  
Db 140 SWCLQSLTLFVLP-----NGQAHKPSGARVPSLSVQLSLAMHTWYLATMFLFIKDPVNM 195  
Qy 294 LVFEVSELVGGFGTAIVVENNHYPLEKIGDPVWDGHSVQGIHETMNRIRGITDWF 353  
Db 196 VYFLVSAVCGNLLAIIVSLNHNMPVSKIEEAVDMDFFTKQIITGRDVPGLFANWFTG 255  
Qy 354 GLNYQIEHHLWPTLPRHNLTAVSQVEQLCQKHNLPRNPLPHEGLVILLRYLAVERMA 413  
Db 256 GLNYQIEHHLFSPMRNFSKIQPAVETLCKKNVRIHTTGNIETGTA-----EVFSKLN 309  
Qy 414 EKQPA-----GKA 421  
Db 310 EVSKAASKMGKA 321

## RESULT 5

US-10-029-756-27  
; Sequence 27, Application US/10029756  
; Patent No. US20020108147A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.  
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
; DELTA 6-DESATURASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/029,756  
; FILING DATE: 21-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/934,254  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Presser, Leopold  
; REGISTRATION NUMBER: 19,827  
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-10-029-756-27

Query Match 20.2%; Score 461; DB 12; Length 452;  
Best Local Similarity 27.6%; Pred. No. 2e-39;  
Matches 123; Conservative 73; Mismatches 189; Indels 60; Gaps 10;  
Qy 11 LQLEQTYDVSAVNFHFGGAEIENYQGRDADAFVMVHFOEADPKLRMPKINPSFEL 70  
Db 25 ISIQGVYDCSRWAAEHGPEVPLLSLAGQDVTDAFVHPGTAW---RHLDPLFTGYV 81  
Qy 71 PPOAAVNEAQEDFKRLREELIATGMEDASP---LWYSYKISTTLGLGLVGLVLMVQYQW 127  
Db 82 LKDFEVSISDKYRLLNMSRSGIFKKGHIMMTFVGVAVVMAAIVTVGLVASESVGVH 141  
Qy 128 FIGAVLLGMHYQMGWLSHDICHQTEKRNWNNLVGLVFGNGLOGESVTCCKDRNNAH 187  
Db 142 MLCGALLGLLWIAQYVGHDSGHYQVMPTRGYNRTITQIAGNLLIGISATWKNTHA 201  
Qy 188 SATNVQGHDPDIDNPLPLAWS-----DDVTRASPISRKLQFOQYYFLVICIL 236  
Db 202 LACNSLDYDPLDQHIFPFAVSTRFNSITSFVGRVLKDFEVARFLVSYQHTYYVPMIF 261  
Qy 237 LR---FWFCQCVLTVRSKDRNQFVRSYKKEAIGLALHTWLKALFLHFFMPSILTS 293  
Db 262 GRVNLFIQTFFLLTLTRDVPDR-----ALNLMGIAVETWTFPLF----- 300  
Qy 294 LVFEVSELVGGFGTAIVVF-----NNHYPLEK-IGDPVWDGHSVQGIHETM 341  
Db 301 -VSCLPNWPERFGVFLISFAVTAIQHVOTLNHFSGDYVGPDP---KGNWFEKTKGTID 357  
Qy 342 IRRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCQKHNLPRN---PLPHE 397



Db 358 ITCPPMDWFGGQFQLEHHLFRLPRGLRKIAPLARDLCKKHGHPYRSFGFWDDANV 417  
Qy 398 GLVILLRYLAVFARMAEKQAPGAKAL 422  
Db 418 RTITLRDAVAOARDLNSAPCPKKL 442

RESULT 6  
US-10-262-617-1  
; Sequence 1, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 09/048,888  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CD1  
US-10-262-617-1

Query Match 19.4%; Score 443.5; DB 9; Length 445;  
Best Local Similarity 29.8%; Pred. No. 1.3e-37;  
Matches 123; Conservative 61; Mismatches 160; Indels 69; Gaps 14;

Qy 11 LOLMEQYDVSANWFHPGGAETIENYOGDRATDAFWMH-----FQAFDKLRMPKINP 66  
Db 39 LVITERRYDISRWQAHRPGGSRLLGHGAEDATDAFRAHODLNFVRKFLQPLLIGELAP 98  
Qy 67 SFELPPQAAVNEAO--EDFRKLREELIATGMFDSPLWYSYKISTITLGLVGLYFLMVQY 124  
Db 99 --EPPSODGPLNAOLVEDFRALHOAAEDMKLFDASPTFFAFLLGHILAMEVLAWLL---- 152  
Qy 125 QMYFIG-----AVLLGHYQQMGWLSHDICHQHTFKNRNNNVLGLVFGNGLOGFS 175  
Db 153 -IYLLPGWPSALAAFLAISQAQSNCLQHDHGHASTFKKSWNNHVAQKFMVQOLKGFS 211  
Qy 176 VTCWKDRHNAHSATNVOGHPDIDNLPPLAWSDDVTRASPISRKLIQFOQ--YYFLV- 232  
Db 212 AHWNFRHFQHAKPNIFHKDPDVTAPVFLGESSVEYGGKKRYLPYNOOHLFFELIG 271  
Qy 233 --ICILLRFIWCFOCLTVRSCLKORDNOFYRSQYKKEAIGLALHW-----TKALFHL 283  
Db 272 PPLTLVNF-----EVENLAY-----MLVCQWADLLWAASYAREFL 309  
Qy 284 FFMPSI-LTSLLVFVS-ELVGGFGIAIVFPMNHPLEKIGDPVWDGH-----GFSVQIH 337  
Db 310 SYLPFYGPVGLLFFAVRVLESFWFVWITQMNHPKE-----IGHEKRDWVSSQLA 362  
Qy 338 ETMNIIRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVQOLCOKHNL 390  
Db 363 ATCNVPSLFTNWFSGHLNFQIEHHLFPRMPCRNLRKISPYVIELCKHNL 415

RESULT 7  
US-10-029-756-5  
; Sequence 5, Application US/10029756  
; Patent No. US20020108147A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/029,756  
FILING DATE: 21-Dec-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,254  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-029-756-5

Query Match 19.0%; Score 433.5; DB 12; Length 448;  
Best Local Similarity 29.8%; Pred. No. 1.5e-36;  
Matches 121; Conservative 67; Mismatches 167; Indels 51; Gaps 14;

Qy 11 LOLMEQYDVSANWFHPGGAETIENYOGDRATDAFWMHFEADFKLRMPKINPSEL 70  
Db 25 ISIQGKAYDVSQWYKDHDPGSGFPLKSLAGQEVDAFVAFHPASTW---KNLDKFTGYTL 81  
Qy 71 PPQAAVNEAOEDFRKLREELIATGMFDSPLWYSYKISTITLGLVGLYFLMVQY 124  
Db 82 -KDYSVSEVSKDYKRLVFEFSKMGLYDKKHMFATLCF---IAMLFAMSVYGVLFCEGV 137  
Qy 125 QMYFIGAVLLGHYQQMGWLSHDICHQHTFKNRNNNVLGLVFGNGLOGFSVTCWKDRHN 184  
Db 138 LVHLFSGLCMFLWTQSGWIGHAGYMWVSDSRNLKPMGFIAAANCLSGISIGMWKWNHN 197  
Qy 185 AHSATNVOGHPDIDNLPPLAWS-----EDDVTRASPISRKLIQFOQYFLV 232  
Db 198 AHHIACNSLEYDPPLOQYIPFLVWSKFGSTSHYEKRLTFDS--LSRFFVYQHWTFP 256  
Qy 233 ICILLRFIWCFOCLTVRSCLKORDNOFYRSQYKKEAIGLALHWTLLKALHLEFFMPSILTS 292  
Db 257 IMCAARLNMVYQSLI---MLTKRNVSYRAQ---ELLCG-----LVFSIW--PLLVS 301  
Qy 293 LL-----VFFVSELVGGFGIAIVF--MNHVPLE-KIGDPVWDGHGFSVQIHWETNIRR 344  
Db 302 CLPNWGERIMEFVIASLSVTGMQOQVQFSLNHFFSSSVYVGKP--KGNWFEKOTDGTLDISC 359  
Qy 345 GIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVQOLCOKHNL 390  
Db 360 PPWMDWFGGSGQFQIEHHLFPRMPCRNLRKISPYVIELCKHNL 405

RESULT 8

US-10-262-617-3  
; Sequence 3, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS  
; FILE REFERENCE: PF-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 09/048,888  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CD1  
US-10-262-617-3

Query Match 18.8%; Score 430; DB 9; Length 444;  
Best Local Similarity 28.7%; Pred. No. 3.4e-36;  
Matches 118; Conservative 67; Mismatches 172; Indels 54; Gaps 14;  
QY 11 LQMEQTYDVSAMVNFHGGAEIENYQGRDATDAFVMMHFOEAFDK-----LKRMPK 63  
DB 36 LVDRKYNISEFTRRHPGGSRVISHYAGQDATDPFAFINKGLVKYKYNLSLIGELSP 95  
QY 64 INPSFELPPOAAVNEAQEDFRKLREELIATGMFDASPLWYSYKI-----STTLGLGV 115  
DB 96 EQSPFE---PTKNKELTDEFRELATVERMGLMKANHVFFLLYLLHLLDGAALTLWV 152  
QY 116 LGYFLMVOYQMYFVIGAVLLGMHYQMGWLSHDICHQHTFKNRNNNLV-GLVFGNGLQGF 174  
DB 153 FG----TSFLPFLLCALLSAVQAQAGWLQHDYGHLSVSTKWNHLLHFVIGH-LKGA 207  
QY 175 SVTCWKDRINAHSAFNVQGHDPDIDNPLPLAWSDDV--TRASPISRKLIQF---QQY 229  
DB 208 PASWNHMFQHHAKPNCERKDPDI-NMHPFSFALGKILSVELGKOKKMTYNNHQHYF 266  
QY 230 FLV---ICILLRFVQCVLTVRSLKDRDNQFYRSQYKKEAIGLALHWTLKALFHLFFM 286  
DB 267 FLIGPPALLPLVFWYI-----FYFVIQRKKWYDLAWMITFYVFFLYV 311  
QY 287 P--SILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDGHSVQGIHETMNI 344  
DB 312 PLLGLKAFGLGFFIVRFLESNNFVWVTQNMHPIHDHNDMD---WVSTQLQATCNVHK 368  
QY 345 GIITDFFGGLNVOIEHLLWPTLPRNHLTAVSQVEQLCKOKHNLPRN-PL 394  
DB 369 SAFNDWFSGLNFOIEHLLFPTMPRNLHKKVAPLVQSLCAKHGIEYQSRPL 419

RESULT 9  
US-10-191-513A-9  
; Sequence 9, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295, US D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613

; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (432)...(432)  
; OTHER INFORMATION: Xaa - Unknown or other at position 432  
US-10-191-513A-9  
Query Match 18.7%; Score 426; DB 9; Length 432;  
Best Local Similarity 28.0%; Pred. No. 8.6e-36;  
Matches 118; Conservative 72; Mismatches 178; Indels 54; Gaps 12;  
QY 11 LQMEQTYDVSAMVNFHGGAEIENYQGRDATDAFVMMHFOEAFDK-----LKRMPK 63  
DB 24 LVDRKYNISEFTRRHPGGSRVISHYAGQDATDPFAFINKGLVKYKYNLSLIGELSP 83  
QY 64 INPSFELPPOAAVNEAQEDFRKLREELIATGMFDASPLWYSYKI-----STTLGLGV 115  
DB 84 EQSPFE---PTKNKELTDEFRELATVERMGLMKANHVFFLLYLLHLLDGAALTLWV 140  
QY 116 LGYFLMVOYQMYFVIGAVLLGMHYQMGWLSHDICHQHTFKNRNNNLVGLVFGNGLQGF 175  
DB 141 FG----TSFLPFLLCALLSAVQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKAS 196  
QY 176 VTCWKDRINAHSAFNVQGHDPDIDNPLPLAWSDDVTRASPI--SRKLIQF-----QQ 227  
DB 197 ANWNHMFQHHAKPNCERKDPDI-NMHPFSFALGKILSVELGKOKKMTYNNHQHYF 251  
QY 228 YFLV-ICILLRFVQCVLTVRSLKDRDNQFYRSQYKKEAIGLALHWTLKALFHLFFM 286  
DB 252 YFLIGPPLLPVFWYI-----IVHKNWVDLAWAVSYIRFFITYI 298  
QY 287 P--SILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDGHSVQGIHETMNI 344  
DB 299 PFYIGLALLFLNFIREFLESNNFVWVTQNMHPIHDHNDMD---WFS-SQLTATCNVEQ 355  
QY 345 GIITDFFGGLNVOIEHLLWPTLPRNHLTAVSQVEQLCKOKHNLPRNPLPHEGLVILLR 404  
DB 356 SFNDWFSGLNFOIEHLLFPTMPRNLHKKVAPLVQSLCAKHGIEYQSRPL 419  
QY 405 YL 406  
DB 416 SL 417

RESULT 10  
US-10-191-513A-38  
; Sequence 38, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295, US D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610

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; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (432)...(432)
; OTHER INFORMATION: Xaa - Unknown or other at position 432
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa - Unknown or other at position 458
US-10-191-513A-38

Query Match      18.7%; Score 426; DB 9; Length 465;
Best Local Similarity 28.0%; Pred. No. 9.5e-36;
Matches 118; Conservative 72; Mismatches 178; Indels 54; Gaps 12;

Qy 11 LQMEQYDVSANVNFHGGAEIENYOGSDATDAFVMVHFOEAFDK-----LKRMPK 63
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 LVDRKYNINSEFTRRHGGSRVISHYAGODATDPFVAFHINKGLVKYKMNLLIGELSP 83
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 64 INPSFELPPQAAVNEAQEDFRKLREELIATGMFDASPLWYSYKI-----STTLGLGV 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 84 EQPSFE---PTKNKELTDEFRELRTATVERMGLMKANHVFFLLYLLHLLLDGAAWLTLMV 140
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 116 LGYFLMVQYMYFTGAVLLGHMYQOMGLSHDICHQHTFKNRNNNVLGLVFGNGLOQFS 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 FG-----TSFLPFLCAVLLSAVQAAGWLQHDYGLHSYRKPKNHLVHKEFVIGHLKAS 196
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 176 VTCWKDRHNAHNSATNVQGHDPDIDNLPPLAWSDDVTRASPI---SRKLIQF-----QQ 227
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 ANMNNHRHFQHAKEPNIFHKDPDYNMLHVFVLGE-----WQPIEYGGKKLYLPYNHQHE 251
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 228 YFELV-ICILRFIWCFCVLTVRSLKDRDNQFYRSQYKKEAIGLALHWTLKALFLHFFM 286
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 YFFLIGPFLIPMTFOYQIINTM-----IVHKNWDLAWAVSYIRFFITIYI 298
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 P--SILTSLLVFFVSELVGGFGIAIVFMNHPYLEKIGDPVWDGHSVQGIHETMNR 344
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 PFYIGLALLFLNIRFLESWFVWYTMNHPVLEIDQEAIED--WFS-SQLTATCNVEQ 355
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 345 GIITDFGGLNYQIEHHLWPTLPRLNLTAVSYQVEQLCQKHNLNPLRPHLEGVLILLR 404
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 SFENDWFGSLNFQIEHHLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIR 415
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 405 YL 406
   |
Db 416 SL 417

RESULT 11
US-10-191-513A-12
; Sequence 12, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610

Query Match      18.2%; Score 416; DB 9; Length 444;
Best Local Similarity 28.5%; Pred. No. 9.9e-35;
Matches 117; Conservative 66; Mismatches 174; Indels 54; Gaps 14;

Qy 11 LQMEQYDVSANVNFHGGAEIENYOGSDATDAFVMVHFOEAFDK-----LKRMPK 63
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 LVDRKYNINSEFTRRHGGSRVISHYAGODATDPFVAFHINKGLVKYKMNLLIGELSP 95
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 64 INPSFELPPQAAVNEAQEDFRKLREELIATGMFDASPLWYSYKI-----STTLGLGV 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 EQPSFE---PTKNKELTDEFRELRTATVERMGLMKANHVFFLLYLLHLLLDGAAWLTLMV 152
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 116 LGYFLMVQYMYFTGAVLLGHMYQOMGLSHDICHQHTFKNRNNNVLGLVFGNGLOQFS 174
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 FG-----TSFLPFLCAVLLSAVQAAGWLQHDYGLHSYRKPKNHLHHLHFVIGH-LKGA 207
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 175 SVTCWKDRHNAHNSATNVQGHDPDIDNLPPLAWSDDV--TRASPISRKLIQF---QQY 229
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 PASMNNHMFQHAKEPNIFHKDPDIDNLPPLAWSDDV--NMHPFFALGKILSVELGKQKKYMPYNHQHKE 266
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 230 FLV---ICILRFIWCFCVLTVRSLKDRDNQFYRSQYKKEAIGLALHWTLKALFLHFFM 286
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 FLIGPPALLPLFYQWYI-----FYFVIQRKKWVDLAWMITFVVRFFLTIV 311
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 P--SILTSLLVFFVSELVGGFGIAIVFMNHPYLEKIGDPVWDGHSVQGIHETMNR 344
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 PLLGLKAFGLFFIVRFLSNWFWVWYTMNHPHIDHIDRNMND--WVSTQLLATCNVHK 368
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 345 GIITDFGGLNYQIEHHLWPTLPRLNLTAVSYQVEQLCQKHNLNPLRPN-PL 394
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 369 SAFNDWFGSLNFQIEHHLFPTMPRHNLHKTAPLVKSLCAKHGIEYQEKPL 419

; Sequence 42, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa - Unknown or other at position 444
US-10-191-513A-42
```

Query Match 17.6%; Score 402.5; DB 9; Length 444;  
Best Local Similarity 28.2%; Pred. No. 2.5e-33;  
Matches 116; Conservative 65; Mismatches 175; Indels 55; Gaps 14;

QY 11 LQLEQTYDYSANWFHGGAEIENYQGRDATDAFMMHFQEAQFADK-----LKRMPK 63  
DB 36 LVDRKYNINSEFRRHPPGGSRVISHYAGQADDPFAFHINKGLVKYKNSLLIGELSP 95  
QY 64 INSEFELPPAAVNEAQEDFRKLREELIATGMDASPLWTSYKI-----STTIGLV 115  
DB 96 EQPSFE-----PTNKELTDEFELRATVERGLMAKANHVFFLLYLLHLLLDGAWLTLW 151  
QY 116 LGYFLVQYOMYFIVGAVLLGHYQOMGLSHDICHHTQFKNRNNLV-GLVFGNGLOGF 174  
DB 152 FG-----TSFLPFLLCVALLSAVQAQAGLQHDGSLVSFTSKNHLHLHFVIGH-LKGA 206  
QY 175 SVTCWDRHNAHSATNVQGHDPDIDNLPPLAWSEDDV--TRASPISRKLIQF---QOYY 229  
DB 207 PASWNNHMFQHHAKPNCFRKDPDI-NMHPFFALGKILSVELGKQKKYMPYNHQHYF 265  
QY 230 FLV---ICILLRIWFOCVLTVRSKDRDNQYRSQYKKEAIGLALHWTLKALFLHFFM 286  
DB 266 FLIGPPALLPLXYQWYI-----EYFVIQRKKWVDLAWMITFYVRFPLTYV 310  
QY 287 P--SILTSLLVFFVSELVGGFGIAIVYMMHYPLEKIGDPVMDGHGFSVGOIHETMNR 344  
DB 311 PLGLKAFGLFFIVFLESNWFVWVTQMNHPIHIDHRNMD---WVSTQLLATCNVHK 367  
QY 345 GIITDFFGGLNYQIEHHLWPTLRNHLTAVSVQVQOLCOKHNLPRN-PL 394  
DB 368 SAFNDWFSGLHNFQIEHHLWPTLRNHYKHVAPLVOSLCAKRIEYQSKPL 418

RESULT 13  
US-09-967-477B-4  
; Sequence 4, Application US/09967477B  
; Patent No. US30020156254A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiao Qiu  
; APPLICANT: Haiping Hong  
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL  
; FILE REFERENCE: BZ-001  
; CURRENT APPLICATION NUMBER: US/09/967,477B  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/236,303  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/297,562  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 439  
; TYPE: PRT  
; ORGANISM: Thraustochytrium sp.  
US-09-967-477B-4

Query Match 16.3%; Score 372; DB 9; Length 439;  
Best Local Similarity 29.2%; Pred. No. 3.8e-30;  
Matches 121; Conservative 69; Mismatches 164; Indels 60; Gaps 21;

QY 18 YDVSANWFN-HPGGAEI---IENYQGRDATDAFMMHFQ--EAFDKLRMPKINPS---- 67  
DB 33 YDAT---NEKHPGGSIIINTEGEACVATQAYREPHQSGKADKYLSPLKLDASKVES 89  
QY 68 -FELPPQAVNEAQEDFRKLREELIATGMDASPLWTSYKI-STTIGLVGLVFLAYQY- 125  
DB 90 REFAKEQARRDAMTDYAAFARELVAEAGYFDPSPHMYRVVVEIVAFALFSLWMSKASP 149  
QY 126 -MYFTGAVLLGHYQOMGLSHDICHHTQFKNRNN--NNLVGLVFGNGLOGFSVTCWKR 182  
DB 150 TSLVLGVNMGIAQRCGVMNHEM-GHGSFTGVILWDRMCEFFYGVGC-GMSGHYWKNO 207

Query Match 13.7%; Score 312.5; DB 9; Length 356;  
Best Local Similarity 30.2%; Pred. No. 4.5e-24;  
Matches 87; Conservative 48; Mismatches 122; Indels 31; Gaps 8;

QY 129 IGAVLLGMHYQOMGLSHDICHHTQFKNRNNLVGLVFGNGLOGFSVTCWKRNNHNS 188  
DB 13 ITAFVLATSDQAQAGLQHDYGLSVYRKPRNHLVHKFVIGHLKAGANMNNHRRFQHHA 72  
QY 189 ATNVQGHDPDIDNLPPLAWSEDDVTRASPI--SRKLIQF-----QOYYFLV-ICILLRF 239  
DB 73 KPIHFHDPDNNMLHVFVLGE---WQPIEYKCKKLKYLKYPNNHQHEVFFLIGPPLIPM 127  
QY 240 IWCFOCVLTVRSKLD-RDNQYRSQYKKEAIGLALHWTLKALFLHFWPMSILTSLLVFFV 298  
DB 128 YFOYQIIMTIVHKNWVDLAWAVSYIRFTTIPFYGILGALLFLNFRFLESHWFMV-- 185  
QY 299 SELVGGFGIAIVYMMHYPLEKIGDPVMDGHGFSVGOIHETMNRRIITDWFPGGLNYQ 358  
DB 186 -----VTQMNHIVMEIDQEAIRD--WFS-SQLTATCNVEQSFNDWFSGLHNFQ 231

QY 183 HNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASP--ISRKLIQFOOYYFL-VICILLRF 239  
DB 208 HSKHHAAPNRLEHADVDLNTLPLVAFNERVVRKVPKPSLLALWLRLVQAYLFAVPVSCLLIGL 267  
QY 240 IWCFOCVLTVRSKDRDNQYRSQYKKEAIGLALHWTLKALFLHFWPMSIL-----TSL 294  
DB 268 GW-----TLYLHPRYMLRTRHMEFV-----WIFARYIGFSLMAGALGYSPTSGV 313  
QY 295 VFFVSELVGGFGI-AIVVFM-----NHYPLEKIGDPVMDGHGFSVGOIHETMNT-RRGI 346  
DB 314 MYLCS-----FGLGCIIVFLQFAVSHTHLPVTNPEDQL---HWLEYAADH-TVNISTKSW 364  
QY 347 ITDFFGGLNYQIEHHLWPTLRNHLTAVSVQVQOLCOKHNLPRNPLPHGGLV 400  
DB 365 LVTWMSNLNFAQIEHHLWPTLRNHLTAVSVQVQOLCOKHNLPRNPLPHGGLV 417

RESULT 14  
US-10-191-513A-18  
; Sequence 18, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (294)....(294)  
; OTHER INFORMATION: Xaa = Unknown or other at position 294  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (320)....(320)  
; OTHER INFORMATION: Xaa = Unknown or other at position 320  
US-10-191-513A-18

Query Match 13.7%; Score 312.5; DB 9; Length 356;  
Best Local Similarity 30.2%; Pred. No. 4.5e-24;  
Matches 87; Conservative 48; Mismatches 122; Indels 31; Gaps 8;

QY 129 IGAVLLGMHYQOMGLSHDICHHTQFKNRNNLVGLVFGNGLOGFSVTCWKRNNHNS 188  
DB 13 ITAFVLATSDQAQAGLQHDYGLSVYRKPRNHLVHKFVIGHLKAGANMNNHRRFQHHA 72  
QY 189 ATNVQGHDPDIDNLPPLAWSEDDVTRASPI--SRKLIQF-----QOYYFLV-ICILLRF 239  
DB 73 KPIHFHDPDNNMLHVFVLGE---WQPIEYKCKKLKYLKYPNNHQHEVFFLIGPPLIPM 127  
QY 240 IWCFOCVLTVRSKLD-RDNQYRSQYKKEAIGLALHWTLKALFLHFWPMSILTSLLVFFV 298  
DB 128 YFOYQIIMTIVHKNWVDLAWAVSYIRFTTIPFYGILGALLFLNFRFLESHWFMV-- 185  
QY 299 SELVGGFGIAIVYMMHYPLEKIGDPVMDGHGFSVGOIHETMNRRIITDWFPGGLNYQ 358  
DB 186 -----VTQMNHIVMEIDQEAIRD--WFS-SQLTATCNVEQSFNDWFSGLHNFQ 231



Result No.	Query			Description				
	Score	Match	Length	ID				
c	1	62.4	4.3	449	9	US-10-191-513A-37	Sequence 37, Appl	
	2	62.4	4.3	473	9	US-10-191-513A-36	Sequence 36, Appl	
	3	62.4	4.3	655	9	US-10-191-513A-3	Sequence 3, Appl	
	4	62.4	4.3	864	9	US-10-191-513A-13	Sequence 13, Appl	
	5	62.4	4.3	1335	9	US-10-191-513A-1	Sequence 1, Appl	
	6	62.4	4.3	1928	9	US-10-262-617-4	Sequence 4, Appl	
	c	7	62.4	4.3	1972	10	US-09-822-849A-485	Sequence 485, App
		8	58.6	4.0	1474	9	US-10-102-806-232	Sequence 232, App
		9	58.6	4.0	1685	9	US-10-191-513A-6	Sequence 6, Appl
	10	58.6	4.0	1843	9	US-10-191-513A-7	Sequence 7, Appl	
	11	58.6	4.0	2257	9	US-10-191-513A-8	Sequence 8, Appl	
	c	12	52	3.6	347	9	US-09-736-457-355	Sequence 355, App
		13	52	3.6	347	9	US-09-902-941-355	Sequence 355, App
		14	52	3.6	347	9	US-09-796-692-4558	Sequence 4558, Ap
	c	15	52	3.6	347	9	US-09-849-626-355	Sequence 355, App
	c	16	52	3.6	347	9	US-10-017-754-355	Sequence 355, App
	c	17	52	3.6	347	9	US-10-040-662-4558	Sequence 4558, Ap
	c	18	52	3.6	1717	9	US-10-262-617-2	Sequence 2, Appl
	19	51.8	3.5	1059	9	US-10-156-761-1580	Sequence 1580, Ap	

---

1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGCTTTGGGGAGGT 1182



## RESULT 5

US-10-191-513A-1  
; Sequence 1, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardi  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-1

Query Match 4.3%; Score 62.4; DB 9; Length 1335;  
Best Local Similarity 59.7%; Pred. No. 3.5e-06;  
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
  
QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGGAGGT 1182  
DB 1075 CAGCTCCTGCCACATGCAATGTCACAAAGTCTGCCTTCAATGACTGGTTCAGTGGACAC 1134  
  
QY 1183 CTTAACTATCAGATTGAGCACCATCTTTCCCAACGATGCCAGACACCACTTGAACACT 1242  
DB 1135 CTCAACTCCAGATTGAGCACCATCTTTTCCCAACGATGCCCTCGACACAATTTACCAAAA 1194  
  
QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298  
DB 1195 GTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCGTGGCATAGTACCAAGTCCAA 1250

## RESULT 6

US-10-262-617-4  
; Sequence 4, Application US/10262617  
; Publication No. US2003007747A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DELTA-5 DESATURASE HOMOLOGS  
; FILE REFERENCE: PP-0494-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/262,617  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 2002-09-30  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 1928  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CB1  
US-10-262-617-4

Query Match 4.3%; Score 62.4; DB 9; Length 1928;  
Best Local Similarity 59.7%; Pred. No. 4.4e-06;

Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
  
QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGGAGGT 1182  
DB 1158 CAGCTCAGGCCACATGCAATGTCACAAAGTCTGCCTTCAATGACTGGTTCAGTGGACAC 1217  
  
QY 1183 CTTAACTATCAGATTGAGCACCATCTTTTCCCAACGATGCCAGACACCACTTGAACACT 1242  
DB 1218 CTCAACTCCAGATTGAGCACCATCTTTTCCCAACGATGCCCTCGACACAATTTACCAAAA 1277  
  
QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298  
DB 1278 GTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGTACCAAGTCCAA 1333

## RESULT 7

US-09-822-849A-485/c  
; Sequence 485, Application US/09822849A  
; Patent No. US20020045170A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakar  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6403  
; CURRENT APPLICATION NUMBER: US/09/822.849A  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/195,582  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 598  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 485  
; LENGTH: 1972  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-849A-485

Query Match 4.3%; Score 62.4; DB 10; Length 1972;  
Best Local Similarity 59.7%; Pred. No. 4.5e-06;  
Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1123 CAAATCATGACCAAGAATAATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGGAGGT 1182  
DB 808 CAGCTCAGGCCACATGCAATGTCCCAAGTCTGCCTTCAATGACTGGTTCAGTGGACAC 749  
  
QY 1183 CTTAACTATCAGATTGAGCACCATCTTTTCCCAACGATGCCAGACACCACTTGAACACT 1242  
DB 748 CTCAACTCCAGATTGAGCACCATCTTTTCCCAACGATGCCCTCGACACAATTTACCAAAA 689  
  
QY 1243 GTTATGCCACTTGTAAAGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTCCA 1298  
DB 688 GTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCATGGCATAGTACCAAGTCCAA 633

## RESULT 8

US-10-102-806-232  
; Sequence 232, Application US/10102806  
; Publication No. US20030054421A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103P1C1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881



;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: 60/124,270  
;; PRIOR FILING DATE: 1999-03-12  
;; NUMBER OF SEQ ID NOS: 846  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 232  
;; LENGTH: 1474  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1337)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1359)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1377)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-10-102-806-232

Query Match 4.0%; Score 58.6; DB 9; Length 1474;  
Best Local Similarity 58.2%; Pred. No. 3.8e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCTTAAATCATGACCAAGAAATATGAGACCTTGAAGATTTCATTGACTGGCTTTGGG 1177  
DB 598 GTAGCCAGCTGACAGCCACCTCCACGTTGGAGCAGTCTTCTACAGACTGGTTCAGTG 657  
QY 1178 GAGGTCTTAACTATCATGATGAGCACCACCTTTTCCACGATGCCAGCAAACTTGA 1237  
DB 658 GACACCTTAACTTCCAGATTGAGCACCACCTCTTCCCACTGCCCCGGCAGCAACTTAC 717  
QY 1238 ACACGTGTTATGCCACTTGTTRAGGAGTTTGCAGCAGCAAAATGTTTACCATATGAG 1294  
DB 718 ACAAGATCGCCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 774

RESULT 9  
US-10-191-513A-6  
;; Sequence 6, Application US/10191513A  
;; Publication No. US20030104596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abbott Laboratories  
;; APPLICANT: Mukerji, Pardip  
;; APPLICANT: Leonard, Amanda E.  
;; APPLICANT: Huang, Yung-Sheng  
;; APPLICANT: Tapas, Das  
;; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;; FILE REFERENCE: 6295 US D3  
;; CURRENT APPLICATION NUMBER: US/10/191,513A  
;; CURRENT FILING DATE: 2002-09-25  
;; PRIOR APPLICATION NUMBER: US 09/227,613  
;; PRIOR FILING DATE: 1999-01-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/07422  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: US 08/833,610  
;; PRIOR FILING DATE: 1997-04-11  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 1686  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-191-513A-6

Query Match 4.0%; Score 58.6; DB 9; Length 1686;  
Best Local Similarity 58.2%; Pred. No. 4.2e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCTTAAATCATGACCAAGAAATATGAGACCTTGAAGATTTCATTGACTGGCTTTGGG 1177  
DB 463 GTAGCCAGCTGACAGCCACCTCCACGTTGGAGCAGTCTTCTTACAGACTGGTTCAGTG 522

QY 1178 GAGGTCTTAACTATCATGATGAGCACCACCTTTTCCACGATGCCAGCAAACTTGA 1237  
DB 523 GACACCTTAACTTCCAGATTGAGCACCACCTCTTCCCACTGCCCCGGCAGCAACTTAC 582  
QY 1238 ACACGTGTTATGCCACTTGTTAAGAGATTTCGACGACCAAAATGTTTACCATATGAG 1294  
DB 583 ACAAGATCGCCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 639

RESULT 10  
US-10-191-513A-7  
;; Sequence 7, Application US/10191513A  
;; Publication No. US20030104596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abbott Laboratories  
;; APPLICANT: Mukerji, Pardip  
;; APPLICANT: Leonard, Amanda E.  
;; APPLICANT: Huang, Yung-Sheng  
;; APPLICANT: Tapas, Das  
;; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;; FILE REFERENCE: 6295 US D3  
;; CURRENT APPLICATION NUMBER: US/10/191,513A  
;; CURRENT FILING DATE: 2002-09-25  
;; PRIOR APPLICATION NUMBER: US 09/227,613  
;; PRIOR FILING DATE: 1999-01-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/07422  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: US 08/833,610  
;; PRIOR FILING DATE: 1997-04-11  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7  
;; LENGTH: 1843  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-191-513A-7

Query Match 4.0%; Score 58.6; DB 9; Length 1843;  
Best Local Similarity 58.2%; Pred. No. 4.4e-05;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCTTAAATCATGACCAAGAAATATGAGACCTTGAAGATTTCATTGACTGGCTTTGGG 1177  
DB 620 GTAGCCAGCTGACAGCCACCTCCACGTTGGAGCAGTCTTCTTCAAGCATGGTTCAGTG 679  
QY 1178 GAGGTCTTAACTATCATGATGAGCACCACCTTTTCCACGATGCCAGCAAACTTGA 1237  
DB 680 GACACCTTAACTTCCAGATTGAGCACCACCTCTTCCCACTGCCCCGGCAGCAACTTAC 739  
QY 1238 ACACGTGTTATGCCACTTGTTAAGAGATTTCGACGACCAAAATGTTTACCATATGAG 1294  
DB 740 ACAAGATCGCCCCGCTGGTGAAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 796

RESULT 11  
US-10-191-513A-8  
;; Sequence 8, Application US/10191513A  
;; Publication No. US20030104596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abbott Laboratories  
;; APPLICANT: Mukerji, Pardip  
;; APPLICANT: Leonard, Amanda E.  
;; APPLICANT: Huang, Yung-Sheng  
;; APPLICANT: Tapas, Das  
;; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
;; FILE REFERENCE: 6295 US D3  
;; CURRENT APPLICATION NUMBER: US/10/191,513A  
;; CURRENT FILING DATE: 2002-09-25  
;; PRIOR APPLICATION NUMBER: US 09/227,613  
;; PRIOR FILING DATE: 1999-01-08  
;; PRIOR APPLICATION NUMBER: PCT/US98/07422  
;; PRIOR FILING DATE: 1998-04-10

;; PRIOR APPLICATION NUMBER: US 08/833,610  
;; PRIOR FILING DATE: 1997-04-11  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 8  
;; LENGTH: 2257  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-191-513A-8

Query Match 4.0%; Score 58.6; DB 9; Length 2257;  
Best Local Similarity 58.2%; Pred. No. 5e-05; Indels 0; Gaps 0;  
Matches 103; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1118 GTCCTCAATGATGACCAACAAGAAATATGAGACCTGGAGATTTCATTGACTGGCTTTGGG 1177  
DB 1034 CTAGCCAGCTGACAGCCACCTGCAACGTTGGAGCAGTCTCTTCTCAACGACTGGTTCAAGTG 1093  
QY 1178 GAGGTCTTAATCATGATTGAGCACCACCTCTTTCCCAACGATGCCAGCACAACACTTGA 1237  
DB 1094 GACACCTTAATCTTCAGATTGAGCACCACCTCTTTCCCAACGATGCCAGCACAACACTTAC 1153  
QY 1238 ACACCTGTTATGCCACTTCTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGG 1294  
DB 1154 ACAAGATGCCCGCTGCTGAGTCTCTATGTGCCAAGCATGGCATTTGAATACCAGG 1210

## RESULT 12

US-09-736-457-355/c  
;; Sequence 355, Application US/09736457  
;; Patent No. US20020168637A1  
;; GENERAL INFORMATION:

;; APPLICANT: Wang, Tongtong  
;; APPLICANT: Bangur, Chaitanya S.  
;; APPLICANT: Lodes, Michael A.  
;; APPLICANT: Fanger, Gary  
;; APPLICANT: Vedvick, Tom  
;; APPLICANT: Carter, Darrick  
;; APPLICANT: Retter, Marc  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Fan, Liqun  
;; APPLICANT: Wang, Aljun  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
;; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.478C15  
;; CURRENT APPLICATION NUMBER: US/09/736.457  
;; CURRENT FILING DATE: 2000-12-13  
;; NUMBER OF SEQ ID NOS: 1864  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 355  
;; LENGTH: 347  
;; TYPE: DNA  
;; ORGANISM: Homo sapien

US-09-736-457-355

Query Match 3.6%; Score 52; DB 9; Length 347;  
Best Local Similarity 55.6%; Pred. No. 0.00093;  
Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 1133 CCACAAGAAATATGAGACCTGGAGATTTCATTGACTGGCTTTGGGAGGTCTTTAACTATC 1192  
DB 340 CCACCTGCAACGTTGGAGCGCTCCTCTTTTCCAACTGGTTTCCAGCGGCGACCTCAACTTCC 281  
QY 1193 AGATTGAGCAGCATCTTTTCCCAACGATGCCAGCACAACACTTGAACACTGTTATGCCAC 1252  
DB 280 AGATCGAGCACCACCTCTTCCCAAGAGTCCGAGACACAACACTAGACCGGGTGGCCCGCG 221  
QY 1253 TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGTCGACGATTATTTCACAG 1312  
DB 220 TGGTCAAGTCGCTGTGTGCCAAGCAGCGCCTCAGCTACGAAGTGAAGCCCTTCTCCTACCG 161

## RESULT 13

US-09-902-941-355/c  
;; Sequence 355, Application US/09902941  
;; Patent No. US20020172952A1  
;; GENERAL INFORMATION:

;; APPLICANT: Henderson, Robert A.  
;; APPLICANT: Wang, Tongtong  
;; APPLICANT: Watanabe, Yoshihiro  
;; APPLICANT: Johnson, Jeffrey C.  
;; APPLICANT: Retter, Marc W.  
;; APPLICANT: Marnerakis, Margarita  
;; APPLICANT: Carter, Darrick  
;; APPLICANT: Fanger, Gary R.  
;; APPLICANT: Vedvick, Thomas S.  
;; APPLICANT: Bangur, Chaitanya S.  
;; APPLICANT: McNabb, Andria  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.478C17  
;; CURRENT APPLICATION NUMBER: US/09/902,941  
;; CURRENT FILING DATE: 2001-07-10  
;; NUMBER OF SEQ ID NOS: 2002  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 355  
;; LENGTH: 347  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens

US-09-902-941-355

Query Match 3.6%; Score 52; DB 9; Length 347;  
Best Local Similarity 55.6%; Pred. No. 0.00093;  
Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 1133 CCACAAGAAATATGAGACCTGGAGATTTCATTGACTGGCTTTGGGAGGTCTTTAACTATC 1192  
DB 340 CCACCTGCAACGTTGGAGCGCTCCTCTTTTCCAACTGGTTTCCAGCGGCGACCTCAACTTCC 281  
QY 1193 AGATTGAGCAGCATCTTTTCCCAACGATGCCAGCACAACACTTGAACACTGTTATGCCAC 1252  
DB 280 AGATCGAGCACCACCTCTTCCCAAGAGTCCGAGACACAACACTAGACCGGGTGGCCCGCG 221  
QY 1253 TTGTTAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGTCGACGATTATTTCACAG 1312  
DB 220 TGGTCAAGTCGCTGTGTGCCAAGCAGCGCCTCAGCTACGAAGTGAAGCCCTTCTCCTACCG 161

## RESULT 14

US-09-796-692-4558/c  
;; Sequence 4558, Application US/09796692  
;; Publication No. US20020198362A1  
;; GENERAL INFORMATION:

;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Algate, Paul A.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND T  
;; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
;; FILE REFERENCE: 2077.001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; CURRENT FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201



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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:22:56 ; Search time 74.2248 Seconds  
(without alignments)  
6036.458 Million cell updates/sec

Title: US-09-857-583-1  
Perfect score: 1461  
Sequence: 1 gaatttcacatctccttg.....tccaaattttacattacc 1461

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73.8	5.1	1617	2	US-08-834-655-1
2	73.8	5.1	1617	3	US-08-834-033A-1
3	73.8	5.1	1617	3	US-09-363-574-1
4	73.8	5.1	1617	4	US-09-363-526-1
5	73.8	5.1	1617	4	US-09-330-235-17
6	62.4	4.3	449	4	US-09-439-261-38
7	62.4	4.3	449	4	US-09-227-613-37
8	62.4	4.3	473	4	US-09-439-261-37
9	62.4	4.3	473	4	US-09-227-613-36
10	62.4	4.3	655	4	US-09-439-261-3
11	62.4	4.3	655	4	US-09-227-613-3
12	62.4	4.3	864	4	US-09-439-261-12
13	62.4	4.3	864	4	US-09-227-613-13
14	62.4	4.3	1335	4	US-09-439-261-1
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16	58.6	4.0	1686	4	US-09-439-261-6
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18	58.6	4.0	1843	4	US-09-439-261-7
19	58.6	4.0	1843	4	US-09-227-613-7
20	58.6	4.0	2257	4	US-09-439-261-8
21	58.6	4.0	2257	4	US-09-227-613-8
22	50.8	3.5	7218	1	US-08-232-463-14
23	48.6	3.3	1684	2	US-08-831-570-1
24	48.6	3.3	1684	2	US-08-831-575-1
25	48.6	3.3	1685	1	US-08-366-779-4
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28	38.2	2.6	2220	4	US-09-134-001C-749	Sequence 749, App
c 29	36.8	2.5	1632	4	US-09-134-001C-728	Sequence 728, App
c 30	36.8	2.5	12597	4	US-09-705-299-12	Sequence 12, Appl
31	36.2	2.5	914	4	US-09-475-316A-24	Sequence 24, Appl
32	36.2	2.5	1702	4	US-08-934-254-26	Sequence 26, Appl
c 33	36.2	2.5	3369	2	US-08-619-198-2	Sequence 2, Appl
c 34	36.2	2.5	4170	2	US-08-619-198-4	Sequence 4, Appl
c 35	36.2	2.5	5192	2	US-08-619-198-8	Sequence 8, Appl
c 36	36.2	2.5	5198	2	US-08-619-198-1	Sequence 1, Appl
37	35	2.4	14636	4	US-09-173-914-6	Sequence 6, Appl
38	34.8	2.4	4223	4	US-09-541-782-5	Sequence 5, Appl
39	34.8	2.4	4223	4	US-09-723-820-5	Sequence 5, Appl
c 40	34.4	2.4	991	1	US-08-232-463-19	Sequence 19, Appl
c 41	34.4	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
42	34.2	2.3	244	1	US-08-686-878A-43	Sequence 43, Appl
43	34.2	2.3	1224	4	US-09-134-001C-562	Sequence 562, App
44	34	2.3	4330	3	US-09-310-293-1	Sequence 1, Appl
45	34	2.3	4330	4	US-09-579-376-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-834-655-1  
; Sequence 1, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUITZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834.655  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RAE-VENTER, BARBARA  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CGNE.124.0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 328-4400  
; TELEFAX: (650) 328-4477  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1617 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-08-834-655-1

Query Match 5.1%; Score 73.8; DB 2; Length 1617;  
Best Local Similarity 47.5%; Pred. No. 1.1e-11;  
Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;



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QY 1188 CTATCAGATTGACACATCTTTTCCCAAGAGTGCACGACACAACTTGAACACTGTTAT 1247  
DB 1249 CTATCAGATGAGCACCACCTTTTCCCTTCGATGCTCGCCACCAACTTTTCAAAAGATCCA 1308  
QY 1248 GCCACTTGTAAAG 1260  
DB 1309 GCCTGCTGCGAG 1321

## RESULT 3

US-09-363-574-1  
; Sequence 1, Application US/09363574  
; Patent No. 6136574  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERT, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/363,574  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WARD, MICHAEL R.  
; REGISTRATION NUMBER: 38,651  
; REFERENCE/DOCKET NUMBER: CGAB-202 USA  
; TELEPHONE: (415) 433-4150  
; TELEFAX: (415) 433-8716  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1617 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; US-09-363-574-1

Query Match 5.1%; Score 73.8; DB 3; Length 1617;  
Best Local Similarity 47.5%; Pred. No. 1.1e-11;  
Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;  
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DB 531 TGTCTCGGCTGGCTTTTGGTCTCTTCTGGCAGCAGTCGGATGGTTGGCTCAGCACT 590  
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DB 591 TTTTGCATCAGAGGCTTTCAGGACCGTTCCTGGGGTGTCTTTTTCGGGCCCTCTCTGG 650  
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DB 651 GAGGTGCTGCCAGGGCTTCTCGCTCGTGGTGAAGGACAGCAACAACACTCACCACG 710  
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QY 740 TGCAGACAATCTCAACAATTTATCTCAGGATTCATGCTGTTATGCTCTATTCAGATGGC 799  
DB 769 GAGTGAGCATGCTGGAGATGTTCTCGGATGTCAGATGAGGAGTGCACCCGATGTG 828  
QY 800 AACATGTTCAATGGACATTT-----CATGTTACCATTTCTCTCCG 836  
DB 829 GTCGCGTTTCATGCTCTGAACAGACGCTGTTTACTTCCCATTTCTCTGTTTGGCG 888  
QY 837 TCTCTGCTGCTTCTTCAGTCAATCATTTTGTAGTACAGATGCCAATCATTTATTTATGA 896  
DB 889 TCTCTGCTGCTGCTCCAGTCCATTTCTTTGTGCTGCTTAACGCTCAGGCCCAAGCC 948  
QY 897 CTATTACAGAAAT-----ACTGCGATTATGAACAGGTTGGTCTCTCTTTCACCTGGC 950  
DB 949 CTCGGGGCGCGTGTGCCCATCTCTGTTGGTCGAGCAGCTGCTGCTGCGATGCACTGGAC 1008  
QY 951 TTGCTCATTTGGTCAATTTGT---ATTTCCTACCCGATTTGGTCAACTAGAATAATTTCTT 1007  
DB 1009 CTGCTACCTCGCCACCATGTTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTGTACTT 1068  
QY 1008 CTTGTTTCTCATCTTTGTTGAGGTTTCTCTGCTCTCTCATGTAGTTACTTTCAATCATTA 1067  
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QY 1248 GCCACTTGTAAAG 1260  
DB 1309 GCCTGCTGCGAG 1321

## RESULT 4

US-09-363-526-1  
; Sequence 1, Application US/09363526  
; Patent No. 6410288  
; GENERAL INFORMATION:  
; APPLICANT: KNUTZON, DEBORAH  
; APPLICANT: MURKERT, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
; STREET: 2001 FERRY BUILDING  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:









RESULT 14  
US-09-439-261-1  
; Sequence 1, Application US/09439261  
; Patent No. 6428990  
; GENERAL INFORMATION:

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Job time : 79.2248 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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(Without alignments)  
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Perfect score: 1461  
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Scoring table: IDENTITY\_NUC  
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- 8: gb.pl.\*
- 9: gb.pr.\*
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- 13: gb.un.\*
- 14: gb.vi.\*
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- 18: em.in.\*
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- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
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- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	658.2	45.1	38060	3	CET13F2 Z81122 Caenorhabd
5	348.2	23.8	1463	3	AF031477 Caenorhab
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7	120.2	8.2	30748	3	CEW08D2 Z70271 Caenorhabd
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9	94.2	6.4	1374	8	AF465282 Mortierel
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17	83	5.7	1590	8	AB020032 Mortierel
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19	82.4	5.6	1578	6	AX481946 Sequence
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22	82.4	5.6	15430	6	AX481635 Sequence
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24	82.4	5.6	17752	6	AX481638 Sequence
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26	74.2	5.1	1546	6	AB052086 Mucor cir
27	73.8	5.1	1617	6	AR080598 Sequence
28	73.8	5.1	1617	6	AR098439 Sequence
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ALIGNMENTS

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LOCUS  
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complete cds.  
ACCESSION  
AF114440  
VERSION  
AF114440.1 GI:4235625  
SOURCE  
Caenorhabditis elegans.  
ORGANISM  
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Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE  
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AUTHORS  
Watts,J.L. and Browse,J.  
TITLE  
Isolation and characterization of a Delta 5-fatty acid desaturase

JOURNAL from Caenorhabditis elegans  
MEDLINE Arch. Biochem. Biophys. 362 (1), 175-182 (1999)  
PUBMED 99117288  
9917342  
REFERENCE 2 (bases 1 to 1461)  
AUTHORS Watts, J.L. and Browne, J.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-1998) Institute of Biological Chemistry,  
Washington State University, Clark Hall, Pullman, WA 99164-6340,  
USA

## FEATURES

Location/Qualifiers

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/gene="fat-4"

/codon\_start=1

/product="delta5-fatty acid desaturase"

/protein\_id="AADI3294.1"

/db\_xref="gi:4235626"

/translation="MVLREQHEPFFIKIDGKWCQIDDAVLRSHPGSAITTYKNMDA  
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VAMQGLDHLIEFHAEHQDFKNRYINDLASFYVGNLQFSSGQWKEQNHVHAATNV  
GRGDLDLPVYATVAEHLNNYSQDSWYMTLFRQWQHWMTFMLPELRLSWLLQSIIFY  
SOMPTHYDYRYNTAIYEQVGLSLHAWSLQOLYFLPDWSTRIMFPLVSHLVGGFLLS  
HWVFNHYSVKFKALSSNIMSYACLOLWTRNMRPGRFIDWLWGLNAYQIEHHLFT  
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BASE COUNT

426 a 292 c 273 g 470 t

ORIGIN

Query Match 100.0%; Score 1461; DB 3; Length 1461;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAATTTCAATCCTCTTGGTGGTCCACCGCTGTGTATCAAAATGGTATTACGAGAGCA 60  
QY 61 GAGCATGAGCCATCTTCATTAATAATGATGAAATGGTGCAATGGATGACCATGCTGTC 120  
DB 61 GAGCATGAGCCATCTTCATTAATAATGATGAAATGGTGCAATGGATGACCATGCTGTC 120  
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DB 241 AAAGAGTCCCTTACACAAGAACGAGATCCAGATATTAAGATGACCCCAATCAAGGA 300  
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DB 301 ATTGATGATGTGAACATGGGAACCTTCAATATTTCTGAGAAACGATCTGCCCAATAAAT 360  
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RESULT 2

AF078796

LOCUS

DEFINITION

complete cds.

ACCESSION

AF078796 1344 bp mRNA linear INV 11-DEC-1998  
Caenorhabditis elegans delta 5 fatty acid desaturase (des-5) mRNA,  
complete cds.

DB 481 CAATACCACACATATTTCTTCCATCAGCTATTTCTAATGGGAGTTGCGTGGCAACAATTTG 540  
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Caenorhabditis elegans.
Caenorhabditis elegans
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Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lewis, M., Griffiths, G., Lazarus, C.M.
and Stobart, A.K.
Functional identification of a fatty acid delta5 desaturase gene
from Caenorhabditis elegans
FEBS Lett. 439 (3), 215-218 (1998)
95059458
9845325
2 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lazarus, C.M., Griffiths, G. and
Stobart, A.K.
Direct Submission
Submitted (16-JUL-1998) Biological Sciences, University of Bristol,
Woodland Road, Bristol BS8 1UG, UK
Location/Qualifiers
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RESULT 3  
AX020906  
LOCUS  
DEFINITION Sequence 2 from Patent WO9933958.

linear DNA 1344 bp PAT 07-SEP-2000



Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Tl3f2>

**IMPORTANT:** This sequence is not the entire insert of clone Tl3F2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone Tl3F2 is at 1 in this sequence. The true left end of Clone W0802 is at 37953 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence AL022473. The end of this sequence (37953..38060) overlaps with the start of sequence Z70271.

**IMPORTANT:** This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers

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/chromosome="IV"

/clone="Tl3F2"

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#### FEATURES

source

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CDS

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cdna EST yk99g7.5 comes from this gene

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QY		



960307: Dual-authors: June Swinburne & Rachael Ainscough For a graphical representation of this sequence and its analysis see: <http://www.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=W08D2>

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

# FEATURES

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Location/Qualifiers

1. 30748

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gene

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cDNA EST yk10d12.5 comes from this gene

cDNA EST yk5f9.3 comes from this gene

cDNA EST yk10d12.3 comes from this gene

cDNA EST yk40h11.5 comes from this gene

cDNA EST yk131g11.3 comes from this gene

cDNA EST yk131g11.5 comes from this gene

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cDNA EST yk122a12.5 comes from this gene

cDNA EST yk248h3.5 comes from this gene

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/gene="W08D2.6"

/gene="W08D2.6"

/note="predicted using GeneFinder"

contains similarity to Pfam domain: PF01391 (Collagen

triple helix repeat (20 copies)), Score=73.1,

E-value=1.9e-18, N=2; PF01484 (Nematode cuticle collagen

N-terminal domain), Score=67.8, E-value=7.3e-17, N=1

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 Db 1284 TATAGAAATTCGGATGCTACTCATATATTTCCAGCTTTCCACGAAGGATCTCTCAGGCT 1343  
 Qy 217 TATCAATGGCTGACAGAAATGAAAAAGAGTGCCTACACAGAACACAGATCCAGAT 276  
 Db 1344 TATAAGCACTTGACCTTCGTGAAAAGCAGCG-----AGAGCAGATGAATTCCTTGAG 1397  
 Qy 277 ATTAAGGATGACCACTCAAGGAATGATGATGATGATGATGATGATGATGATGATGAT 336  
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 Qy 337 GAGAAAGGATGCGCCCAATTAATAAAGTTTCACTGATCATGATGATGATGATGATGATG 396  
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 Db 1578 ATTATGCAATTTGCAATTTTATCTTCACTATCTTGGATGATATTAATCTTGCATGTTA 1637  
 Qy 517 ATGGGAGTTGGTGGCAACATGGGATGGTAAATCATGATGATGATGATGATGATGATG 576  
 Db 1638 TTAGCACTTGATGCGCAACATTCGGATGGTTTACACATGATGATGATGATGATGATG 1697  
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 Db 1758 TTTTCAAGAGATTGGTGGAGGACAG 1784

RESULT 8  
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 ACCESSION AF139720  
 VERSION AF139720.1 GI:5639723  
 KEYWORDS  
 SOURCE Euglena gracilis.  
 ORGANISM Euglena gracilis  
 Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.  
 Wallis, J.G. and Browse, J.  
 TITLE The Delta8-desaturase of Euglena gracilis: an alternate pathway for synthesis of 20-carbon polyunsaturated fatty acids  
 JOURNAL Arch. Biochem. Biophys. 365 (2), 307-316 (1999)  
 MEDLINE 99262077  
 PUBMED 10328826  
 REFERENCE 2 (bases 1 to 1275)  
 AUTHORS Wallis, J.G. and Browse, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-MAR-1999) Institute of Biological Chemistry,

Washington State University, 441 Clark, Pullman, WA 99164-6340, USA  
 Location/Qualifiers  
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 BASE COUNT 294 a 326 c 327 g 328 t

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 Qy 592 TACAATGATTTGGCCAGCTATTTGTTGGAACATTTTACAAGGATTTCTCATCTGGTGGT 651  
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AX058840 2160 bp DNA linear PAT 17-JAN-2001

Sequence 11 from Patent WO0075341.

AX058840

AX058840.1 GI:12311157

Ceratodon purpureus.

Ceratodon purpureus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
Bryopsida; Dicranales; Dicranales; Ditrichaceae; Ceratodon.

1 (bases 1 to 2160)

Helnz,E., Stymne,S., Lee,M., Girke,T., Sperling,P. and  
Zachringer,U

\_g(d)6-acetylase and \_g(d)6-desaturase from ceratodon purpureus

Patent: WO 0075341-A 11 14-DEC-2000;

BASF AKTIENGESSELLSCHAFT (DE)

Location/Qualifiers

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800 AACATGTTTCATTGGACATT-----CATGTTTACCATTCCCTCCG 836

759 GTCGCGCTTCATGGTCTTTAACGACACCTGGTTCTACTTTCCCATCTCTCGTTGGCCG 818

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AX058840 2160 bp DNA linear PAT 17-JAN-2001

Sequence 11 from Patent WO0075341.

AX058840

AX058840.1 GI:12311157

Ceratodon purpureus.

Ceratodon purpureus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

1 (bases 1 to 2160)

Helnz,E., Stymne,S., Lee,M., Girke,T., Sperling,P. and Zaehringer,U

\_g(d)6-acetylase and \_g(d)6-desaturase from ceratodon purpureus

Patent: WO 0075341-A 11 14-DEC-2000;

BASF AKTIENGESSELLSCHAFT (DE)

Location/Qualifiers

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Best Local Similarity		48.0%; Pred. No. 3.3e-11;							
Matches 369; Conservative		0; Mismatches 384; Indels 15; Gaps 3;							
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QY	978	ACCCGATTGGTCA	ACTAGATAATGTTCTCTT	TGTTTCTCATCTT	GTGGAGGTTTCCCT		1037		
Db	1325	GCTCCCGGATG	GAACACCACTGTT	TATGGATGGTGGT	CAGCGAGCTCATGCT	CTGTTTCCCT	1384		
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RESULT 11	CPU250735	2160 bp	mRNA	linear	PLN 21-JUN-2000
LOCUS	CPU250735				
DEFINITION	Ceratodon purpureus mRNA for delta 6-fatty acid desaturase.				
ACCESSION	AJ250735				
VERSION	AJ250735.1				
KEYWORDS	cytochrome b5; delta 6-fatty acid desaturase; desaturase.				

SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL TITLE	JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS	JOURNAL TITLE	FEATURES	source
Ceratodon purpureus.	Sperling, P., Lee, M., Girke, T., Zahringer, U., Stymne, S. and Heinz, E.	A bifunctional delta-fatty acyl acetylase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily	Eur. J. Biochem. 267 (12), 3801-3811 (2000)				
Ceratodon purpureus	Sperling, P.	Direct Submission	20307617				
Eukaryota; Viridiplantae; Bryophyta; Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.		Submitted (28-OCT-1999)	10848999				
1 (bases 1 to 2160)		Submitted fuer Allgemeines Botanik, Universitaet Hamburg, Ohnhorststrasse 18, D-22609 Hamburg, GERMANY					
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CDS		159. .1721					
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ORIGIN							
Query Match	6.4%;	Score 93.6;	DB 8;	Length 2160;			
Best Local Similarity	48.0%;	Pred. No. 3.3e-11;					
Matches 369;	Conservative 0;	Mismatches 384;	Indels 15;	Gaps 3;			
QY	498	TCTTCATCAGCTATTCTTAATGGGAGTGTGCGTGGCAACAAATGGGATGGTGTAAATCCATGA	557				
Db	848	TCTGTTATCAGCAGCTTTGATGGCGTGTGTTTATTCAACAGTGGCGATGGTGTCTCACGA	907				
QY	558	ATTGCGACATCATCAGTTGTTCAAAAACAGATACTACAATGATTTGCCAGCTATTTTCGT	617				
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SOURCE	Mortierella alpina.	1003
ORGANISM	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae; Mortierella.	1003
REFERENCE	1 (bases 1 to 1374)	1013
AUTHORS	Xing, L., Li, M., Liu, L., Hu, G. and Zhang, L.	1013
TITLE	Expression of Mortierella alpina delta 6-fatty acid desaturase gene in Saccharomyces cerevisiae	1013
JOURNAL	Unpublished	1013
REFERENCE	2 (bases 1 to 1374)	1013
AUTHORS	Xing, L., Li, M., Liu, L., Hu, G. and Zhang, L.	1013
TITLE	Direct Submission	1013
JOURNAL	Submitted (26-SEP-2000) Department of Microbiology, Nankai University, 94 Weijin Road, Tianjin 300071, P.R. China	1013
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AUTHORS	Xing, L., Li, M., Liu, L., Hu, G. and Zhang, L.	1290
TITLE	Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA	1290
JOURNAL	Unpublished	1290
REFERENCE	2 (bases 1 to 1374)	1290
AUTHORS	Xing, L., Li, M., Liu, L., Hu, G.	1290
TITLE	Direct Submission	1290
JOURNAL	Submitted (04-JAN-2002) Microbiology, Nankai University, Weijing road 94th, Tianjin 300071, China	1290
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## ORIGIN

Query Match 6.1%; Score 89.2; DB 8; Length 1374;  
Best Local Similarity 48.4%; Pred. No. 3.6e-10;  
Matches 396; Conservative 0; Mismatches 388; Indels 34; Gaps 4;

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## RESULT 15

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ACCESSION AF465283  
VERSION AF465283.1 GI:18483178  
KEYWORDS Mortierella alpina.  
SOURCE Mortierella alpina  
ORGANISM Mortierella alpina

Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;  
Mortierellaceae; Mortierella.  
1 (bases 1 to 1947)  
AUTHORS Liu, L., Li, M., Hu, G. and Xing, L.  
TITLE Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA Unpublished  
JOURNAL 2 (bases 1 to 1947)  
AUTHORS Xing, L., Liu, L., Li, M. and Hu, G.  
TITLE Direct Submission  
JOURNAL Submitted (04-JAN-2002) Microbiology, Naikai University, Weijing road 94th, Tianjin 300071, China  
FEATURES  
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Matches 396; Conservative 0; Mismatches 388; Indels 34; Gaps 4;

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## SUMMARIES

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2	1344	92.0	1344	20	AAAX8961
3	348.2	23.8	1463	20	AAAX76589
4	108.8	7.4	1275	21	AAAS1233
5	93.6	6.4	2160	22	AAAF25734
6	82.4	5.6	2012	22	AAAF26040
7	73.8	5.1	1374	21	AAAZ7129
8	73.8	5.1	1374	22	AAAF25234
9	73.8	5.1	1617	19	AAV63624

10	73.8	5.1	1617	20	AAAX00889	Mortierella alpina
11	73.8	5.1	1617	21	AAA09430	M. alpina delta-6
12	62.4	4.3	655	19	AAV63638	Contig 2153526 enc
13	62.4	4.3	655	20	AAV00905	Human desaturase g
14	62.4	4.3	655	20	AAV82637	Contig 2153526 enc
15	62.4	4.3	655	21	AAA49934	Human delta-5-desa
16	62.4	4.3	655	21	AAA09448	Human contig DNA e
17	62.4	4.3	655	21	AAA14589	Nucleotide sequenc
18	62.4	4.3	864	21	AAA49944	Putative human des
19	62.4	4.3	1335	21	AAA49932	Human delta-5-desa
20	62.4	4.3	1335	22	AAF25236	Nucleotide sequenc
21	62.4	4.3	1686	22	AAF63836	Human secreted pro
22	62.4	4.3	1856	22	AAH15766	Human cDNA sequenc
23	62.4	4.3	1946	22	AAH17649	Human cDNA sequenc
24	62.4	4.3	1972	24	ABK35347	Human cDNA encodin
25	62.4	4.3	2080	22	AAK94270	Human full-length
26	62.4	4.3	2236	22	AAK94234	Human full-length
27	62.4	4.3	2614	21	AAK76207	Human ORFX ORF1762
28	62.4	4.3	2629	22	AAH99666	Human protein enco
29	62.4	4.3	4203	21	AAA90955	Human fatty acid d
30	62.4	4.3	4205	21	AAA90952	Human fatty acid d
31	62	4.2	1335	22	AAI66599	Rat fatty acid des
32	62	4.2	1335	22	AAI19402	Rat delta-6-desatu
33	61.2	4.2	1467	22	AAF25730	C. purpureus delta
34	61.2	4.2	2040	22	AAF25729	Lipid modification
35	59.8	4.1	451	22	AAH50922	P patens lipid met
36	59.8	4.1	451	22	AAH56909	P patens lipid met
37	59.8	4.1	451	22	AAH56929	Human cDNA clone (
38	58.6	4.0	560	22	AAH05343	Human delta-6-desa
39	58.6	4.0	1335	22	AAI19403	Human breast and o
40	58.6	4.0	1474	21	AAF21845	Human polynucleoti
41	58.6	4.0	1575	24	ABE90108	Contig 2511785 enc
42	58.6	4.0	1686	19	AAV63641	Human desaturase g
43	58.6	4.0	1686	20	AAAX00908	Contig 2511785 enc
44	58.6	4.0	1686	20	AAV82640	Human delta-5-desa
45	58.6	4.0	1686	21	AAA49937	

## ALIGNMENTS

RESULT 1  
AAAS1232  
ID AAAS1232 standard; cDNA; 1461 BP.  
AC AAAS1232;  
XX  
DT 26-SEP-2000 (first entry)  
DE  
DE C. elegans fatty acid delta-5-desaturase coding sequence.  
XX  
XX Fatty acid delta-5 desaturase; polyunsaturated; oil; seed;  
KW infant formula; dietary supplement; fat-4; ss.  
XX  
XX Caenorhabditis elegans.  
OS  
XX  
XX Key Location/Qualifiers  
FT CDS 43..1386  
FT /tag= a  
FT /product= Fatty\_Acid\_delta-5-desaturase  
XX  
XX WO200034439-A1.  
XX  
XX 15-JUN-2000.  
XX  
XX 06-DEC-1999; 99WO-US28655.  
XX  
XX 07-DEC-1998; 98US-0111301.  
XX  
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
XX Browse JA, Wallis JG, Watts JL;  
XX

DR WPI; 2000-431293/37.  
 XX P-PSDB; AAY96721.  
 XX Purified protein having desaturase activity, useful for creating a  
 PT double-bond between two carbons  
 XX  
 XX Claim 6; Fig 6B; 74pp; English.  
 CC This cDNA encodes Caenorhabditis elegans fatty acid delta-5 desaturase.  
 CC The cDNA was isolated from cosmid rfi3f2 and the gene, designated Fat-4.  
 CC The sequence is useful for recombinant production of the enzyme and for  
 CC generating transformed host cells and transgenic plants. The desaturase  
 CC can be used for creating a double-bond between two carbons. In  
 CC particular, the enzyme is useful for producing polyunsaturated fatty  
 CC acids and for generating enzyme-specific antibodies useful for  
 CC identifying desaturases. Oil-seed plants may be engineered to incorporate  
 CC the enzyme, so that the plants produce seed oil rich in fatty acids. The  
 CC fatty acids could be incorporated usefully into infant formula, foods of  
 CC all kinds, dietary supplements, nutraceutical and pharmaceutical  
 CC formulations.  
 XX  
 XX Sequence 1461 BP; 426 A; 292 C; 273 G; 470 T; 0 other;  
 Query Match 100.0%; Score 1461; DB 21; Length 1461;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAATTTCAATCTCTTGGTCCACCGCTGTGATATCAAAATGGTATACGAGAGCAA 60  
 DB 1 GAATTTCAATCTCTTGGTCCACCGCTGTGATATCAAAATGGTATACGAGAGCAA 60  
 QY 61 GAGCATGAGCATCTTCAATTAATAATGATGGAATGGTCTCAAAATGGAGATGCTGTC 120  
 DB 61 GAGCATGAGCATCTTCAATTAATAATGATGGAATGGTCTCAAAATGGAGATGCTGTC 120  
 QY 121 CTGAGATCACATCCAGTGGTGTGCAATTAATTAATAATGATGGAATGGTCTCAAAATGGAGATGCTGTC 180  
 DB 121 CTGAGATCACATCCAGTGGTGTGCAATTAATTAATAATGATGGAATGGTCTCAAAATGGAGATGCTGTC 180  
 QY 181 GTATTCCACACATCCATCTAGTGTCTTAAGAAGCGGTATCAATGGCTGACAGATTGAAA 240  
 DB 181 GTATTCCACACATCCATCTAGTGTCTTAAGAAGCGGTATCAATGGCTGACAGATTGAAA 240  
 QY 241 AAAGAGTGCCCTCACAGAAGACAGATCCAGATTAATAGGATGACCCCAATCAAGGA 300  
 DB 241 AAAGAGTGCCCTCACAGAAGACAGATCCAGATTAATAGGATGACCCCAATCAAGGA 300  
 QY 301 ATTGATGATGTGAACATGGGAACCTTCAATATTTCTGAGAAACGATCTGCCCAATTAAT 360  
 DB 301 ATTGATGATGTGAACATGGGAACCTTCAATATTTCTGAGAAACGATCTGCCCAATTAAT 360  
 QY 361 AAAAGTTTCACTGATCTACGATGCGGATGCGTGCAGAGGACATTATGGATGGATCTCCT 420  
 DB 361 AAAAGTTTCACTGATCTACGATGCGGATGCGTGCAGAGGACATTATGGATGGATCTCCT 420  
 QY 421 TTGTTCTACATTAAGAAAATCTTGAACAAATCTTCAAAATCTTTTGGCATTTCTACCTT 480  
 DB 421 TTGTTCTACATTAAGAAAATCTTGAACAAATCTTCAAAATCTTTTGGCATTTCTACCTT 480  
 QY 481 CAATACCACACATATTATCTTCCATCAGCTATTCTAATGGGAGTTGGCGCAACAATTG 540  
 DB 481 CAATACCACACATATTATCTTCCATCAGCTATTCTAATGGGAGTTGGCGCAACAATTG 540  
 QY 541 GGATGGTAAATCCATGAATTCGCACATCATCATGTTGTTCAAAAACAGATACATAATGAT 600  
 DB 541 GGATGGTAAATCCATGAATTCGCACATCATCATGTTGTTCAAAAACAGATACATAATGAT 600  
 QY 601 TTGCCAGCATTTTCGTTGGAACCTTTTCAAGGATTTCTCATCTGTTGGTGAAGAG 660  
 DB 601 TTGCCAGCATTTTCGTTGGAACCTTTTCAAGGATTTCTCATCTGTTGGTGAAGAG 660  
 QY 661 CAGCACAAATGTGCATACGAGCCACAAATCTTGTGACGAGAGGATCTTGATTTA 720  
 DB 661 CAGCACAAATGTGCATACGAGCCACAAATCTTGTGACGAGAGGATCTTGATTTA 720

DB 661 CAGCACAAATGTGCATACGAGCCACAAATCTTGTGACGAGAGGATCTTGATTTA 720  
 QY 721 GTCCCATCTATGCTACAGTGGCAGACATCTCACAAATTTATCTCAGGATTCATGGGTT 780  
 DB 721 GTCCCATCTATGCTACAGTGGCAGACATCTCACAAATTTATCTCAGGATTCATGGGTT 780  
 QY 781 ATGACTCTATTACAGATGGCAACATGTTTCAATGGACATTCATGTTTACCATTCTCCGTC 840  
 DB 781 ATGACTCTATTACAGATGGCAACATGTTTCAATGGACATTCATGTTTACCATTCTCCGTC 840  
 QY 841 TCGTGGGTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAACTCATATTATGACTAT 900  
 DB 841 TCGTGGGTTCTTCAGTCAATCATTTTGTAGTCAGATGCCAACTCATATTATGACTAT 900  
 QY 901 TACAGAAATCTCGGATTTATGAACAGGTTGGTCTCTCTTGGCACTGGGCTGGCATG 960  
 DB 901 TACAGAAATCTCGGATTTATGAACAGGTTGGTCTCTCTTGGCACTGGGCTGGCATG 960  
 QY 961 GGTCAAATGTATTTCCTACCGGATTTGGTCAACTAGATAATGTTCTTCTCTTCTCAT 1020  
 DB 961 GGTCAAATGTATTTCCTACCGGATTTGGTCAACTAGATAATGTTCTTCTCTTCTCAT 1020  
 QY 1021 CTTGTTGAGGTTTCTCTCTCTCATGTAGTTACTTTCAATCATATTTCAGTGGAGAAG 1080  
 DB 1021 CTTGTTGAGGTTTCTCTCTCTCATGTAGTTACTTTCAATCATATTTCAGTGGAGAAG 1080  
 QY 1081 TTTGCATGAGCTCGAATCATGTCAAATACGCTTCTCTTCAATCATGACCAACA 1140  
 DB 1081 TTTGCATGAGCTCGAATCATGTCAAATACGCTTCTCTTCAATCATGACCAACA 1140  
 QY 1141 AATATGAGACCTGGAAGATTTCAATGAGTGGTCTTGGGAGGTCCTTAACTATCAGATTGAG 1200  
 DB 1141 AATATGAGACCTGGAAGATTTCAATGAGTGGTCTTGGGAGGTCCTTAACTATCAGATTGAG 1200  
 QY 1201 CACCATCTTTTCCCAACGATGCCAGCACAACTTTGAACACTGTTATGCCACTTGTAAAG 1260  
 DB 1201 CACCATCTTTTCCCAACGATGCCAGCACAACTTTGAACACTGTTATGCCACTTGTAAAG 1260  
 QY 1261 GAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTGCAGAGTATTTCACAGGATCTCG 1320  
 DB 1261 GAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTGCAGAGTATTTCACAGGATCTCG 1320  
 QY 1321 CTTGAAATGAGCAATTCGGAATTTTCAAAATGTTGCTGTAAATTTGACTAAAAAGATT 1380  
 DB 1321 CTTGAAATGAGCAATTCGGAATTTTCAAAATGTTGCTGTAAATTTGACTAAAAAGATT 1380  
 QY 1381 GCCTAGATTAAGATTAATTAATCAATTTTATTTTCAATGTTTATCGTGTGTTTAAATTT 1440  
 DB 1381 GCCTAGATTAAGATTAATTAATCAATTTTATTTTCAATGTTTATCGTGTGTTTAAATTT 1440  
 QY 1441 TTCCAAATTTTACCATTATCC 1461  
 DB 1441 TTCCAAATTTTACCATTATCC 1461  
 RESULT 2  
 AAX86961  
 ID AAX86961 standard; cDNA; 1344 BP.  
 XX AAX86961;  
 AC AAX86961;  
 XX  
 DT 24-SEP-1999 (first entry)  
 XX  
 DE C. elegans delta 5-fatty acid desaturase encoding cDNA.  
 XX  
 KW Delta 5-fatty acid desaturase; dihomogamma linolenic acid; gene therapy;  
 KW arachidonic acid; cholesterol; polyunsaturated fatty acid; foodstuff;  
 KW dietary supplement; prostaglandin; ss.  
 OS Caenorhabditis elegans.  
 XX  
 PN WO9933958-A2.  
 XX

PD 08-JUL-1999.  
 XX 23-DEC-1998; 98WO-GB03895.  
 XX 29-JUN-1998; 98GB-0014034.  
 PR 23-DEC-1997; 97GB-0027256.  
 XX (UYBR-) UNIV BRISTOL.  
 XX Michaelson L, Napier JA, Stobart K;  
 PI WPI; 1999-444067/37.  
 DR P-PSDB; AAY21850.  
 DR New isolated delta5-fatty acid desaturase enzymes useful in gene  
 PT therapy  
 PT Claim 4; Page 21; 36pp; English.  
 XX The invention provides delta 5-fatty acid desaturases obtained from  
 CC Mortierella alpina and Caenorhabditis elegans. The delta 5-fatty acid  
 CC desaturases catalyze the production of polyunsaturated fatty acids, e.g.  
 CC the conversion of dihomogamma linolenic acid to arachidonic acid. The  
 CC genes can be used in gene therapy as a preventative treatment, e.g. in  
 CC patients suffering from high levels of cholesterol or other conditions  
 CC where administration of polyunsaturated fatty acids may have beneficial  
 CC disease-preventative effects. The polyunsaturated fatty acids can be used  
 CC in foodstuffs or dietary supplements. The delta 5-fatty acid desaturases  
 CC can also be used for the synthesis of prostaglandins or modulation of the  
 CC synthesis. The products can also be used for detection and diagnosis. The  
 CC present sequence represents the cDNA encoding the C. elegans delta  
 CC 5-fatty acid desaturase.  
 XX  
 XX Sequence 1344 BP; 396 A; 269 C; 261 G; 418 T; 0 other;  
 SQ

Query Match 92.0%; Score 1344; DB 20; Length 1344;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

43 ATGGTATTACGAGCAAGCAGCATGAGCCATTCTTCATTAAATTTGATGAAATGGTGT 102  
 1 ATGGTATTACGAGCAAGCAGCATGAGCCATTCTTCATTAAATTTGATGAAATGGTGT 60  
 103 CAATTTGACGATGCTCTGATGATCAGATCAGATGAGTGGTGGTGGTGGTGGTGGT 162  
 61 CAATTTGACGATGCTCTGATGATCAGATCAGATGAGTGGTGGTGGTGGTGGTGGT 120  
 163 AATATGGGATGCCACTACCCCTATTCACACATTCCTACCTACCTACCTACCTACCT 222  
 121 AATATGGGATGCCACTACCCCTATTCACACATTCCTACCTACCTACCTACCTACCT 180  
 223 TGGCTGACAGAAATGAAAGAGTGGCTTACACAGAACACAGAGATCCAGATATTAAG 282  
 181 TGGCTGACAGAAATGAAAGAGTGGCTTACACAGAACACAGAGATCCAGATATTAAG 240  
 283 GATGACCCCAATCAAGGAATTTGATGATGATGATGATGATGATGATGATGATGATG 342  
 241 GATGACCCCAATCAAGGAATTTGATGATGATGATGATGATGATGATGATGATGATG 300  
 343 CGATCTGCCCAATTAATAAAGTTTCACTGATCTACCTACCTACCTACCTACCTACCT 402  
 301 CGATCTGCCCAATTAATAAAGTTTCACTGATCTACCTACCTACCTACCTACCTACCT 360  
 403 CTTATGGATGGATCTCTCTTTGTTCTACATTTAGAAAAATTTTCAAAACATCTTCAAA 462  
 361 CTTATGGATGGATCTCTCTTTGTTCTACATTTAGAAAAATTTTCAAAACATCTTCA 420  
 463 CTTTTFGATCTTACCTTCAATACCACACATATTTATCTTCCATFAGCTATTTCAATGG 522  
 421 CTTTTFGATCTTACCTTCAATACCACACATATTTATCTTCCATFAGCTATTTCAATGG 480  
 523 GTTGGTGGCAACAATTTGGATGGTAAATCCATGAATTCGACATCATCATGTTGTTCAA 582

Db 481 GTTGGTGGCAACAATTTGGGATGGTTAATCCATGAATTCGCACATCATCAGTTGTTCAA 540  
 QY 583 AACAGATACATACATATTTGGCAGCTATTTGGTGGAACTATTTTACAGAGATTTCTCA 642  
 Db 541 AACAGATACATACATATTTGGCAGCTATTTGGTGGAACTATTTTACAGAGATTTCTCA 600  
 QY 643 TCTGGTGGTGGAAAGAGCAGCAATGTGCATCCAGCAGCAAAATTTGTTGGAGCA 702  
 Db 601 TCTGGTGGTGGAAAGAGCAGCAATGTGCATCCAGCAGCAAAATTTGTTGGAGCA 660  
 QY 703 GACGGAGATCTTGCATTTAGTCCCATTTCTATGCTACAGTGGCAGAACATCTCAACAATTTAT 762  
 Db 661 GACGGAGATCTTGCATTTAGTCCCATTTCTATGCTACAGTGGCAGAACATCTCAACAATTTAT 720  
 QY 763 TCTCAGGATTCATGGGTTATGACTCTATTCAGATGGCAACATGTTCTATGAGACATTCATG 822  
 Db 721 TCTCAGGATTCATGGGTTATGACTCTATTCAGATGGCAACATGTTCTATGAGACATTCATG 780  
 QY 823 TTACCATTCCTCGTCTCTCGTGGCTTCTTCAGTCAATCAATTTTGTAGTCAGATGCCA 882  
 Db 781 TTACCATTCCTCGTCTCTCGTGGCTTCTTCAGTCAATCAATTTTGTAGTCAGATGCCA 840  
 QY 883 ACTCATTATTATGACTATTACAGAAATGCTGAGTTTATGAACAGGTTGGTCTCTCTTTG 942  
 Db 841 ACTCATTATTATGACTATTACAGAAATGCTGAGTTTATGAACAGGTTGGTCTCTCTTTG 900  
 QY 943 CACTGGGCTTGGTTCATTTGGTTCATTTGTTTCTTACCCGATTTGGTCAACTAGAAATTAATG 1002  
 Db 901 CACTGGGCTTGGTTCATTTGGTTCATTTGTTTCTTACCCGATTTGGTCAACTAGAAATTAATG 960  
 QY 1003 TTCTTCTCTGTTTCTCATCTTGTGGAGGTTTCTGCTCTCTCATGTTAGTTTACATTTCAAT 1062  
 Db 961 TTCTTCTCTGTTTCTCATCTTGTGGAGGTTTCTGCTCTCTCATGTTAGTTTACATTTCAAT 1020  
 QY 1063 CATTATTTCAGTGGAGAGTTTGCATTTGAGCTCGAACATCATGTCAAAATTTAGCTTTGCTTT 1122  
 Db 1021 CATTATTTCAGTGGAGAGTTTGCATTTGAGCTCGAACATCATGTCAAAATTTAGCTTTGCTTT 1080  
 QY 1123 CAAATCATGACCAACAAGAAATATGAGACCTTGGAGATTTCAATGCTTGGTGGAGGT 1182  
 Db 1081 CAAATCATGACCAACAAGAAATATGAGACCTTGGAGATTTCAATGCTTGGTGGAGGT 1140  
 QY 1183 CTTAATCATGACCAACAAGAAATATGAGACCTTGGAGATTTCAATGCTTGGTGGAGGT 1242  
 Db 1141 CTTAATCATGACCAACAAGAAATATGAGACCTTGGAGATTTCAATGCTTGGTGGAGGT 1200  
 QY 1243 GTTATGCCACTTCTTAAAGGATTTGACAGCAGCAAAATGTTTACCATCATGCTGACGAT 1302  
 Db 1201 GTTATGCCACTTCTTAAAGGATTTGACAGCAGCAAAATGTTTACCATCATGCTGACGAT 1260  
 QY 1303 TATTTTCACAGGATTTGGCTTGAATTTGAGCAATTTCCGAAATATTGCAAAATTTGCTGCT 1362  
 Db 1261 TATTTTCACAGGATTTGGCTTGAATTTGAGCAATTTCCGAAATATTGCAAAATTTGCTGCT 1320  
 QY 1363 AAATTTGACTAAAAGATTTGCTAG 1386  
 Db 1321 AAATTTGACTAAAAGATTTGCTAG 1344

RESULT 3  
 AAX76589  
 ID AAX76589 standard; cdna; 1463 BP.  
 XX  
 AC AAX76589;  
 XX  
 XT 11-AUG-1999 (first entry)  
 XX  
 DE Caenorhabditis elegans Delta 6 desaturase Ced6.1 encoding cdna.  
 XX  
 KW Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Ced6.1;  
 KW gamma-linolenic acid; GLA; plant fatty acid; octadecatrienoic acid;  
 KW OPA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;  
 KW hypercholesterolemia; diabetic neuropathy; viral infection; acne;







**Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids**

Claim 1a; Page 54-57; 69pp; German.

This invention describes a novel isolated nucleic acid (I), encoding polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by organisms that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids.

Sequence 2160 BP; 509 A; 481 C; 556 G; 614 T; 0 other;

[illegible]

D	b
Db	1445 CTTCTGGT-----AATGCCAGATTGCGACTCCGCACATCAAAACGAGGGT 1497
Qy	1158 ATTCATTGTACTTGCTTTGGGAGGCTTAATACTATCAGATTGAGCACCATCTTTTCCC AAC 1217           
D	b
Db	1493 GTTTAATGATTGTTCCACGGAGGTCTCAACACAGAGATTGAGCATCATCTATTCCA AC 1552           
Qy	. 1218 GATGCCACGACACA ACTTGA CA CTGTTATTGCCACTTGTTAAAGAGTT 1265 
D	b
Db	1553 GATGCCACGACACA A C TTAATAAAAATTTCTCTCACC TG AGACTTT 1600
R	E S U L T    6
A	A F 2 6 0 4 0
I	D     AAF26040 standard; cdna; 2012 BP.
X	X
A	C     AAF26040;
X	X
D	T    23-APR-2001 (first entry)
X	X
D	E    P . patens delta6-desaturase cDNA.
X	X
K	W   Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
X	W   fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
K	W   agricultural chemical; ds.
X	X
X	X
O	S   Physcomitrella patens.
X	X
F	H   Key Location/Qualifiers
F	T   CDS 319..1896
F	T   /*tag= a
F	T   /product= "delta6-desaturase"
X	X
X	X
P	N   WC200102591-A1.
X	X
P	D   11-JAN-2001.
X	X
X	X
P	F   04-JUL-2000; 2000WO-EF06223.
X	X
P	R   06-JUL-1999; 99US-0347531.
P	R   30-JUN-2000; 2000DE-1030976.
X	X
X	X
P	A   (BADI ) BASF AG.
X	X
P	I   Heinz E, Girke T, Scheffler J, Da Costa Silva EO;
X	X
D	R   WPI: 2001-123117/13.
D	R   P-PSDB: AAB46810.
X	X
P	T   Production of unsaturated fatty acids, useful e.g. in nutrition,
P	T   cosmetics or pharmaceuticals, in organisms transformed with
X	X
P	T   Physcomitrella patens delta-6-desaturase nucleic acid -
X	X
P	S   Claim la; Page 38-41; 49pp; German.
X	X
C	C   This invention describes a novel preparation of unsaturated fatty acids
C	C   (I) by introducing into an organism at least one isolated nucleic acid
C	C   (II) that encodes a polypeptide (III) with Delta6-desaturase activity.
C	C   Organisms that contain at least 1 wt.% (I), on total fatty acid content,
C	C   are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),
C	C   defined in the specification, or its equivalents within the degeneracy of
C	C   the genetic code; or (b) derivatives of the sequence of (a) that encode a
C	C   525 amino acid polypeptide (S2), defined in the specification, or a
C	C   polypeptide with at least 50% homology with (S2) and practically the same
C	C   enzymatic activity. The invention also describes (1) transgenic organisms
C	C   that contain (II); and (2) oils, lipids and fatty acids produced by the
C	C   new method. The oils, lipids and fatty acids produced by the transformed
C	C   organisms are used in human or animal nutrition, cosmetics,
C	C   pharmaceuticals and agricultural chemicals. (III) can also be used, in
C	C   vitro, for increasing the (I) content of triglycerides. The transgenic
C	C   organisms have increased contents of (I), or of (I)-containing
C	C   triglycerides, particularly of gamma-linolenic acid.
X	X
S	Q Sequence 2012 BP: 482 A: 427 C: 553 G: 550 T: 0 other:

Query Match 5.68; Score 82.4; DB 22; Length 1012;  
 Best Local Similarity 46.18; Pred. No. 8.2e-12;  
 Matches 398; Conservative 0; Mismatches 451; Indels 15; Gaps 3;

QY 498 TCTTCCATCAGCTATCTTAATGGGAGTGGTGGCAACAATGGGATGGTTAATCCATGA 557  
 DB 1023 TTTGGCTTACGCTGTATGATGCTGTGTTCACACAGTGGGATGGTATCCCATGA 1082  
 QY 558 ATTCGCACATCATCTAGTTTCAAAAACAGATACATCAATGATTTGGCCAGCTATTCGT 617  
 DB 1083 TTTTCTCCCAATCAGGTGTTTGAGACACGCTGGCTTAATGAAGTTCGCGGTATGTAT 1142  
 QY 618 TGAAGAATTTTACAGAGTCTCATCTGCTGGTGGAAAGACAGCAGACATGTCATCA 677  
 DB 1143 CGCAGACGCGTCTGGGGTTTATGACAGGGTGGTGAAGGAAGCATAACTTCATCA 1202  
 QY 678 CGCAGCACAATATTTGGAGGAGACGAGATCTTGATTTAGTCCCATCTATGCTAC 737  
 DB 1203 TGCTGTCCAAATGAATGCCATCAGATTTACCAACCAATTTGATGAAGATATTGATCTCT 1262  
 QY 738 AGTGGCAGAACATCTCAACAATATTCTCAGGATTCATGGGTTATGACTCTATTCAGATG 797  
 DB 1263 CCCCCTCATTTGCCGAGCAAGGACATCTGCGCACAGTTGAGAATAAGACATTC--TTG 1320  
 QY 798 GCAACATGTTTCATGGACATTCATGTTACCATCTCCGCTCTCGTGGCTTCTTCAGTC 857  
 DB 1321 CGAATCCTCAATACCAGCATCTGTTCTTCATGGGCTGTATTATTTTCGCGCTGTGTAGT 1380  
 QY 858 AATCATTTTGTAGTCAGATGCAACTATTATTATGACTATTACAGAAATCTCGGAT 917  
 DB 1381 TGCTCTTTTGGAGCTGGAGATATCTCTACAGAGTGTCTCACCTGTCGACAG--GTT 1439  
 QY 918 TTATGAACAGTTGGTCTCTCTTTGACACTGGGCTTGCTCATTTGGTCAATTTGATTTCC 977  
 DB 1440 GTTGGAGAGGAACTGTTCTGTTTCACTACTTTTGGTTCGTCGGGACACGCTATCT 1499  
 QY 978 ACCGATTTGGTCACTAGATATGTTCTCTCTTTGTTCTCATCTTTGGTGGAGGTTCC 1037  
 DB 1500 TCTCCCTGTTGGAAGCCATTTAGTATGGATGGCGGTGACTGAGCTCATGTCGCGCATG 1559  
 QY 1038 GCTCTCTCATGTAGTTTACTTTCAATCATATTATTCAGTGGAGAACTTTGCAFTGAGTCGAA 1097  
 DB 1560 GCTGGCTTTGTATTGTTACTTACCCACAATGGATGGAGTTTAT-----AA 1607  
 QY 1098 CATCATGTCAATPACGTTGCTTCAATCATATGACCAACAAGAAATATGAGACCTGGAAG 1157  
 DB 1608 TTGCTCTAAAGAAATTCGTGAGTCACAGATCGTATCCACACGGGATATCAAGGAACAT 1667  
 QY 1158 ATTCATTTGACTGCTTTGGGAGGCTTAACTATCATAGATTGACACCATCTTTTCCCAAC 1217  
 DB 1668 ATTCACAGCTGCTTCACTGCTGGTCTTAAACAGCAATAGAGCATCATCTTTTCCCAAC 1727  
 QY 1218 GATGCCACGACAACTTGAACACTGTTATGCCCACCTTTTAAAGAGTTTTCACACGAAA 1277  
 DB 1728 AATGCCAGGCATTAATTTAAACAATAGCACTAGAGTGAGGTTGTTCTGTGAAGAAACA 1787  
 QY 1278 TGGTTTACCATACATGGTGCAGCATTTATTTACAGGATTTCTGCTTGAATTTGAGCAAT 1337  
 DB 1788 CGGTCTGGTGTAGGAAGACGTATCTATTGCTACCGGCACCTTGCAGGTTTGAAGCAAT 1847  
 QY 1338 CGCAATATTGCAATTTGCTGTC 1361  
 DB 1848 GAAGGAAGTCGCGGAGGCTCGGC 1871

RESULT 7  
 AA247129  
 ID AA247129 standard; DNA; 1374 BP.  
 XX  
 AC AA247129;  
 XX  
 DT 28-MAR-2000 (first entry)

XX Fungal delta6-desaturase coding sequence.  
 DE Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;  
 XX transgenic animal; malnutrition; biosynthesis; ds.  
 KW Unidentified.  
 OS WO9961602-A1.  
 PN 02-DEC-1999.  
 XX 28-MAY-1999; 99WO-US12088.  
 XX 29-MAY-1998; 98US-0087578.  
 PR (OHIS ) UNIV OHIO STATE.  
 XX Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;  
 DR WPI; 2000-072619/06.  
 XX P-PSDB; AAY56045.  
 PT Producing essential fatty acids and long-chain polyunsaturated fatty  
 PT acids, for use in nutritional, animal feed and medical formulations -  
 XX Disclosure; Fig 8; 71pp; English.  
 XX The invention relates to a method of generating novel compositions  
 CC comprising animal cells producing essential fatty acids (FAs). The animal  
 CC cells are produced by transforming cells, e.g. embryonic stem cells, with  
 CC nucleic acid encoding heterologous enzymes involved in fatty acid, e.g.  
 CC e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This  
 CC sequence is an example of such a nucleic acid sequence and encodes a  
 CC fungal delta6-desaturase. The essential FAs obtained can be used in  
 CC nutritional formulations or animal feed formulations. The long chain PFAs  
 CC can be used in nutritional formulations, cosmetic formulations or animal  
 CC feed formulations. The products can also be used for producing transgenic  
 CC animals which can be used for producing essential FAs which can be used  
 CC for producing downstream products such as leukotrienes, thromboxanes,  
 CC arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. The  
 CC products can also be used in cell culture. The animal or milk fat  
 CC produced can be administered to treat malnutrition.  
 XX Sequence 1374 BP; 257 A; 387 C; 378 G; 352 T; 0 other;  
 SQ

Query Match 5.18; Score 73.8; DB 21; Length 1374;  
 Best Local Similarity 47.58; Pred. No. 1.4e-09;  
 Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

QY 500 TTCATCAGCTATTTCTAATGGGAGTTCGCTGGCAACAATTTGGGATGGTTAATCCATGAAT 559  
 DB 461 TGCTCTCGGCTGGCTTTTGGTCTGTTCTGGCAGCAGTGGGATGGTTGGCTCAGCACT 520  
 QY 560 TCCGACATCATCTAGTTGTTCAAAAACAGATACATCAATGATTTGGCAGCTATTTCTGTTG 619  
 DB 521 TTTTGGCATCCAGGCTCTCCAGGACCGTTTCTGGGTGATCTTTTGGCGCTCTTTTGG 580  
 QY 620 GAAACATTTTACAGGATTTCTCATCTGTTGGTGAAGAGCAGACACAATCTGCATCAGC 679  
 DB 581 GAGGTGTCTCCAGGCTTCTGCTCTGTTGGTGAAGAGCAGACACAATCTGCATCAGC 640  
 QY 680 CAGCCACAATTTGTTGGAGCAGACGAGATCTTGATTTAGTCCCATCTCTATGCTACAG 739  
 DB 641 CCGCCCCCAACGTCACGCGGAGGATCCCGACATTGA--CACCACCTCTGTTGACCTG 698  
 QY 740 TGGCAGAAATCTCAACAATTTTCTCAGGATTTCAATGGTATGACTCTATTTACAGATGGC 799  
 DB 699 GAGTGAGCATGCTTGGAGATGTTCTCGGATGTCACAGATGAGGAGCTGACCCGCTATG 758  
 QY 800 AACATGTTTATTTGACATTT-----CATGTTACCATTTCTCTCCG 836  
 DB 759 GTCGCGTTTTCATGCTCTGAACAGACCTGTTTACTTCCCATCTCTCTGTTGCGCG 818

QY 837 TCTCTGGGCTTCTTCAGTCAATCTTTTGTAGTCAGATGCCAACTCATTATTATGA 896  
 DB 819 TCTCTCTGGTGGCTTCCAGTCCATCTCTTTGTGCTGCTAACGGTCAGGCCCAAGCC 878  
 QY 897 CTATTACAGAAAT-----ACTGGGATTTATCAACAGCTTGGTCTCTCTTTGGCACTGGGC 950  
 DB 879 CTCGGGCGCGGTGTGCCCATCTCGTTGGTCGAGCAGCTGTGCTTGGATGCTGAC 938  
 QY 951 TTGGTCATTTGGTCAATTTGT---ATTTCCTACCGATGGTCACTAGAAATTAATTTT 1007  
 DB 939 CTGGTACCTGCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTACTT 998  
 QY 1008 CTTGTTTCTCATCTTTGGAGTTTCTCTCTCTCTCATGTAGTACTTTCAATCAATTA 1067  
 DB 999 TTTGGTGTGCGAGCGGTGTGGGAACTTTGTGGGATGCTGTTCTCGCTCAACCAAA 1058  
 QY 1068 TTCAGTGAGAGTTTGGATTCAGCTCGAATCATGTCAAAATTAAGCTTGTCTTCAAT 1127  
 DB 1059 CGGTATGCTGTGATCTCGAAGGAGGCGGTGATATGATTTCTTTCACGAAGCAGAT 1118  
 QY 1128 CATGACCACAGAAATATGACACCTGGAAGATTTCATTGACTGGCTTTGGGAGGCTTAA 1187  
 DB 1119 CATCAGGGTGTGATGTCCACCGGGTCTATTTCGCAACTGGTTTCACGGGTGGATTGA 1178  
 QY 1188 CTATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGCACACACTTTGAACACTGTTAT 1247  
 DB 1179 CTATCAGATCAGCACCATTGTTCCCTTCGATGCTCGCCACACACTTTTCAAGATCCA 1238  
 QY 1248 GCCACTTGTGTAAG 1260  
 DB 1239 GCCTGCTGCGAG 1251

## RESULT 8

AAF25234  
 ID AAF25234 standard; DNA; 1374 BP.  
 AC AAF25234;  
 XX 30-APR-2001 (first entry)  
 DT Nucleotide sequence of a fungal delta6 desaturase.  
 XX  
 DE delta6 desaturase; desaturase gene; elongase gene; fatty acid;  
 KW eicosanoid; nutrition; infant formula; dietary supplement;  
 KW dietary substitute; animal feed; ss.  
 XX  
 OS Mortierella alpina.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1374  
 FT /\*tag= a  
 FT /product=. "delta6 desaturase"  
 XX  
 PN WO200104636-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 11-JUL-2000; 2000WO-US19011.  
 XX  
 PR 12-JUL-1999; 99US-0351525.  
 XX  
 PR (UOVH-) UNIV OHIO.  
 PA  
 XX Kopchick JJ, Kelder B;  
 PI  
 XX WPI; 2001-182622/18.  
 DR P-PSDB; AAB31684.  
 XX  
 PT New compositions comprising cells that express desaturases and  
 PT elongases, for synthesizing essential fatty acids or long-chain  
 PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal

## PT feed formulations

XX Disclosure: Fig 8; 93pp; English.

XX The present sequence encodes a delta6 desaturase. The desaturase  
 CC polynucleotide sequence was used to transfect mammalian cells, to  
 CC produce animal cells expressing a desaturase gene and/or an elongase  
 CC gene. Compositions comprising cells of the invention are useful for  
 CC synthesizing essential fatty acids, their derivatives or downstream  
 CC products, as well as altered levels of long-chain polyunsaturated  
 CC fatty acids and eicosanoids. The compositions are useful in nutritional  
 CC formulae, e.g. infant formula, dietary supplements or dietary  
 CC substitutes for both humans and animals. The compositions are also  
 CC useful in cosmetic or animal feed formulations. Furthermore, the  
 CC compositions may also be used as fat free media or as research reagents.

XX Sequence 1374 BP; 257 A; 386 C; 378 G; 353 T; 0 other;

## Query Match

Best Local Similarity 5.1%; Score 73.8; DB 22; Length 1374;

Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;

QY 500 TTCATACAGCATTTCTAATGGAGTGGTGGCAACAATTTGGATGGTTAATCCATGAAT 559  
 DB 461 TGCTCTCGCTGCGCTTTTGGTCTGTTCTGGCAGCAGTGGTGGTGGTGGTGGTGGT 520  
 QY 560 TCGCACATCAGTGTGTTCAAAACAGATACATGATTTGGCCAGCTATTTCTGTTG 619  
 DB 521 TTTTCATCACCAGGTCTTCCAGGACGTTCTGGGGTGTCTTTTGGCGGCTCTTTGG 580  
 QY 620 GAACTTTTACAGGATTTCTCATCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 679  
 DB 581 GAGGTGCTGCCAGGCTTCTGCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 640  
 QY 680 GAGCCACAATGTTTGGACGAGAGGAGATCTTGATTTAGTCCCATTTCTATGCTACAG 739  
 DB 641 CGGCCCCAACGTCACGCGGAGGATCCGACATTGA--CACCCACCTCTGTTGACCTG 698  
 QY 740 TGGCAGACATCTCAACAATTTCTCAGGATTCATGGGTATGACTCTATTCAGATGCG 799  
 DB 699 GAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCGAGATGAGGAGCTGACCGCATGG 758  
 QY 800 AACATGTTCAATGGACATT-----CATGTTACCATTTCTCTCCG 836  
 DB 759 GTCGGTTCATGGTCTTGAACACGACCTGGTTTACTTCCCATTTCTCTGGTTGCCG 818  
 QY 837 TCTCTCGTGGCTTCTTCAGTCAATCATTTTGTGTAGTCAGATGCCAATCATTTATGA 896  
 DB 819 TCTCTCTGGTGGCTTCCAGTCCATCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 878  
 QY 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGGTTGGTCTCTCTTTGACAC 950  
 DB 879 CTCGGGCGCGGTGTGCCCATCTCGTTGGTCGAGCAGCTGTGCTTGGATGCACTGGAC 938  
 QY 951 TTGGTCAATTTGGTCAATTTGT---ATTTCCTACCGATTTGGTCAACTAGAAATTAAT 1007  
 DB 939 CTGGTACCTGCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGGT 998  
 QY 1008 CTTGTTTCTCATCTTTGGAGGTTTCTCTCTCTCTCATGTAGTACTTTCAATCAATTA 1067  
 DB 999 TTTGGTGTGCGAGCGGTGTGGGAACTTTGTTGGGATGCTGTTCTCGCTCAACCAAA 1058  
 QY 1068 TTCAGTGAGAGTTTGGATTCAGCTCGAATCATGTCAAAATTAAGCTTGTCTTCAAT 1127  
 DB 1059 CGGTATGCTGTGATCTCGAAGGAGGCGGTGATATGATTTCTTTCACGAAGCAGAT 1118  
 QY 1128 CATGACCACAGAAATATGAGACCTGGAAGATTTCATTGACTGGCTTTGGGAGGCTTAA 1187  
 DB 1119 CATCAGGGTGTGATGTCCACCGGGTCTATTTCGCAACTGGTTTCACGGGTGGATTGA 1178  
 QY 1188 CTATCAGATTGAGCACCATTCTTTCCCAACGATGCCAGCACACACTTTGAACACTGTTAT 1247  
 DB 1179 CTATCAGATCAGCACCATTGTTCCCTTCGATGCTCGCCACACACTTTTCAAGATCCA 1238

QY 1248 GCCACTGTGAAG 1260  
 DB 1239 GCCTGCTGCGAG 1251

RESULT 9

AAV63624  
 ID AAV63624 standard; cDNA; 1617 BP.

AC AAV63624;

DT 15-FEB-1999 (first entry)

DE cDNA encoding a delta-6 desaturase enzyme.

KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;  
 malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 cholesterol level; endometriosis; premenstrual syndrome;  
 myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
 OS Mortierella alpina.

FH Key Location/Qualifiers

FT CDS 71..1444

FT /\*tag= a

FT /product= delta-6 desaturase

XX WO9846763-A1.

PN 22-OCT-1998.

PD 10-APR-1998; 98WO-US07126.

PR 11-APR-1997; 97US-0834655.

XX (ABBO ) ABBOTT LAB.

PA (CALJ ) CALGENE LLC.

XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;

PI Thurmond J;

XX WPI; 1998-594582/50.

DR P-PSDB; AAW84137.

XX New isolated fatty acid desaturase enzymes - used for the production  
 of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
 compositions, nutritional compositions, cosmetics or animal feed

PS Claim 1; Fig 3A-E; 165pp; English.

XX The present sequence encodes a Mortierella alpina fatty acid delta-6  
 desaturase enzyme. The enzyme sequence is used in the methods of  
 the invention. The specification describes methods for desaturating a  
 fatty acid and for producing a desaturated fatty acid by expressing  
 increased levels of a desaturase. The present desaturase is an enzyme  
 which introduces a double bond carbons 6 and 7 from the carboxyl end of  
 a fatty acid molecule. The enzyme can be used for desaturating fatty  
 acids. The enzyme can be used to produce polyunsaturated fatty acids,  
 which can be used for treating malnutrition, in pharmaceutical  
 compositions, in cosmetics or in animal feed. The polyunsaturated fatty  
 acids can be used for treating e.g. restenosis after angioplasty,  
 inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes  
 or eczema or reduce blood pressure. They can also be used to inhibit  
 platelet aggregation, cause vasodilation, lower cholesterol levels,  
 inhibit proliferation of vessel wall smooth muscle and fibrous tissue,  
 reduce or prevent gastro-intestinal bleeding and other side effects  
 caused by non-steroidal anti-inflammatory drugs, prevent or treat  
 endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis  
 and chronic fatigue after viral infections, treat AIDS, multiple  
 sclerosis, acute respiratory syndrome, hypertension and inflammatory skin

CC disorders.

XX Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;  
 SQ Query Match 5.1%; Score 73.8; DB 19; Length 1617;  
 Best Local Similarity 47.5%; Pred. No. 1.5e-09;  
 Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;  
 QY 500 TTCCATCAGCTATTCTAATGGGAGTTGCGTGGCAACAATTTGGGATGTTTAAATCAATGAAT 559  
 DB TGTCTCGGCTGCGCTTTTGGGCTCTCTCTGGCAGCAGTCGCGGATGTTGGCTCAGCACT 590  
 QY 560 TCGCACATCATCAGTTGTTCAAAAACAGATACATACATGATTTTGGCCAGCATTTTCGTTG 619  
 DB TTTTGCATCACCAGGCTCTTCCAGGACCGTTTCTCGGGTGATCTTTTCGGGCGCTCTCTTGG 650  
 QY 620 GAAACTTTTACAAAGGATTTCTCATCTGGTGGTGGAAAGAGCAGCAATGTGCATCAGC 679  
 DB 651 GAGGTCTCTGCCAGGCT 710  
 QY 680 CAGCCACAATGTTGTTGGACGAGCAGGATCTTGTATTTAGTCCCATTTCTATGCTACAG 739  
 DB 711 CCGCCCCCAACGTCACGCGGAGGATCCCGACATTGA--CACCCACCTCTGTTGACCTG 768  
 QY 740 TGGCAGAACATCTCAACAATTTATCTCAGGATTTATGCGGTTATGATCTCTATTCAGATGGC 799  
 DB 769 GAGTGAGCATGCGTTTGGAGATGTTCTCGGATGTTCCAGATGAGGAGCTGACCCGATG 828  
 QY 800 AACATGTTTCAATGGACATT-----CATGTTACCATTCCTCCG 836  
 DB 829 GTCGCGTTTTCATGGTCTTGAACAGACCTGGTGTCTTCTCCCATCTCTCTGTTGCCG 888  
 QY 837 TCTCTCGTGGCTTCTCAGTCAATCATTTTGTAGTCAGATGCCAACTCATTTATATGA 896  
 DB 889 TCTCTCTGGTGGCTCCAGTCCATCTCTTGTGCTGCTAACGGTCAGGCCCAAGCC 948  
 QY 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGGTTGGTCTCTCTTTGCACTGGCC 950  
 DB 949 CTCGGCGCGCGTGTGCCCATCTCTGTTGGTCGAGCAGCTGCTGCTTCCGATGCACTGGAC 1008  
 QY 951 TTTGGTCATTGGGTCAATTTGTTTCTTCTACCCGATTTGGTCAACTAGATAATATGTTCTT 1007  
 DB 1009 CTGGTACCTCGCCACCATGTTCTCTGTTCAATCAAGGATCCCGTCAACATGCTGGTGTACT 1068  
 QY 1008 CCTTGTCTCATCTTTGTTGGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1067  
 DB 1069 TTTGGTGTGCGAGCGGTGTGCGAATCTGTTGGCGATGCTGTCTCTGCTCAACCACAA 1128  
 QY 1068 TTGAGTGGAGAAGTTTGCATTTGAGCTCGAACATCATGTCAAATTTACGCTTGTCTTCAAT 1127  
 DB 1129 CGGTATGCTGTGATCTCGAAGGAGGCGGTGATATGATTTTCTTTCACGAGCAGAT 1188  
 QY 1128 CATGACCACAGAAATATGAGACCTGGAAGATTCATTGACTGGCTTTGGGAGGTCTTTAA 1187  
 DB 1189 CATCAGGCTGCTGATGTCACCCGGGTCTATTTCGCAATGGTTCACGGGTGGATTGAA 1248  
 QY 1188 CTATCAGATTGAGCACCACCTTTTCCCAACGATGCCACGACACAACTTGAACACTGTTAT 1247  
 DB 1249 CTATCAGATCGAGCACCACCTTGTTCCTTCGATGCTCGCCGACCACTTTTCAAGATCCA 1308  
 QY 1248 GCACCTGTGTAAG 1260  
 DB 1309 GCCTGCTGTCGAG 1321

RESULT 10

AA00889  
 ID AAX00889 standard; DNA; 1617 BP.  
 XX  
 AC AAX00889;  
 XX 26-MAR-1999 (first entry)  
 XX



OS Mortierella alpina.  
 XX Key Location/Qualifiers  
 FH 71..1443  
 FT CDS /\*tag= a  
 FT /product= delta-6\_desaturase  
 XX  
 XX WO200020602-A2.  
 PN  
 XX 13-APR-2000.  
 XX  
 XX 29-SEP-1999; 99WO-US22686.  
 XX  
 XX 05-OCT-1998; 98US-0103110.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Mukerji P, Huang Y, Parker-barnes JM, Das T;  
 PI WPI; 2000-328935/28.  
 XX P-PSDB: AAY92599.  
 DR  
 XX Novel transgenic insect cells comprising a nucleotide sequences which  
 PT encode delta-6-desaturase or delta-12-desaturase, useful for producing  
 PT polyunsaturated long chain fatty acids, e.g. arachidonic acid  
 XX  
 XX Example 2; Page 144-145; 170pp; English.  
 PS  
 CC The fatty acid desaturases are able to catalyse the conversion of oleic  
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of  
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells  
 CC comprising a nucleotide sequence which encodes a polypeptide comprising  
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6  
 CC desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are  
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated  
 CC from the recombinant insect cells are also claimed. Production of  
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many  
 CC advantages, as insect cells have greatly simplified lipid compositions,  
 CC are not subject to external variable fluctuations, and can easily be  
 CC maintained and manipulated. The oils are used in pharmaceutical  
 CC compositions, infant formulas, dietary supplements or substitutes, and  
 CC cosmetics (all claimed). The PUFA supplements have antiinflammatory,  
 CC antirheumatic, antischismatic, antipsoriatic, osteopathic, cytostatic,  
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,  
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic  
 CC activity.  
 XX  
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;  
 Query Match 5.1%; Score 73.8; DB 21; Length 1617;  
 Best Local Similarity 47.5%; Pred. No. 1.5e-09;  
 Matches 377; Conservative 0; Mismatches 382; Indels 34; Gaps 4;  
 QY 500 TTCATCAGCTATTCTAATGGAGTTCGCTGGCAACAATGGGTGTTAATCCATGAAT 559  
 DB 531 TGCTCTCGCTCGCTTTTGGGTCTGTTCTGGCAGCAGTGGGTGGTTCAGACT 590  
 QY 560 TCGCACATCATCAGTTGTTCAAAAACAGATACATGATTTGGCCAGCTATTTCTGTTG 619  
 DB 591 TTTTTCATCACCAGGTCTTCCAGGACCGTTCCTGGGGTGATCTTTTCGGCGCTCTTGG 650  
 QY 620 GAACTTTTACAAGGATTTCTCATCTGGTGGTGGAAAGAGCAGCAATGTGCATCAG 679  
 DB 651 GAGGTGCTGCCAGGCTTCTGCTCTCGTGGTGGAGGACAGCAACACTCACCAG 710  
 QY 680 CAGCCACAATGTTGTTGACGAGAGCTTTGATTTAGTCCATTTCTATGCTACAG 739  
 DB 711 CCGCCCCCAACCTCCACGCGAGGATCCCGACATTGA--CACCCACCTCTGTTGACCTG 768  
 QY 740 TGGCAGACATCTCAACAATTTCTCAGGATTTCTGAGTTATGACTCTATTAGATGCC 799  
 DB 769 GAGTGAGCATGCTGGAGATGTTCTCGGATCTCCAGATGAGGAGCTGACCCGCATGTG 828

800 AACATGTTCAATGGACATT-----CATGTTACATTCCTCCCG 836  
 829 GTCCGCTTTTCATGCTGCTGAACACAGACCTGGTTTACTTCCCCCATTTCTCTGTTTGGCCG 888  
 837 TCTCTCGTGGCTTTTCAGTCAATCATTTTGTGTAGTCAGATGCCAACTCATATTATTATGA 896  
 889 TCTCTCTGCTGCTCCAGTCCATTTCTTTTGTGCTGCCCTAACGGTCAGGCCCAACAGCC 948  
 897 CTATTACAGAAAT-----ACTGCGATTTATGAACAGGTTGGTCTCTCTTTGCACTGGCC 950  
 949 CTCGGGCGCGGTGTGCCCATCTCGTTGGTCGAGGAGCTGTCGCTTCGGATGCACTGCAC 1008  
 951 TTGGTCAATGGGTCAATGTG---ATTTCCTACCGGATTTGTCACACTAGAATAATGTTCTT 1007  
 1009 CTGGTACCTCGCCACCATGTTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTGTACTT 1068  
 1008 CCTTGTCTCATCTTTGAGGTTTCCCTGCTCTCTCATGTAGTTACTTTCAATCATTA 1067  
 1069 TTTGGTGTGCGAGCGGTGTGCGAAACTTTGTTGGCGATCGTGTCTCGCTCAACCAACAA 1128  
 1068 TTCAGTGGAGAAAGTTTGCATTTGAGCTCGAACATCATGTCAAATTTACGCTTGTCTTCAAAT 1127  
 1129 CGGTATGCTGTGATCTCGAAGGAGGCGGTGATATGATGATTTCTTCACGAGACAGAT 1188  
 1128 CATGACCAAGAATAATATGAGACCTGGAAGATTTCATTTGCTGGTGGGAGGCTCTTAA 1187  
 1189 CATCAGGGTCTGTGATGTCCACCGGTCTATTGTCACACTGGTTTCCAGGTTGATTTGAA 1248  
 1188 CTATCAGATTGAGCACCACCTTTTCCCAAGTGGCCAGCAGACACACTTGAACACTGTTAT 1247  
 1249 CTATCAGATCGAGCACCACCTTTTCCCTTCGATGCTCGCCCAACACTTTTCAAGATCCA 1308  
 1248 GCCACTGTGTAAG 1260  
 1309 GCCTGCTGTGAG 1321

RESULT 12  
 AAV63638  
 ID AAV63638 standard; cDNA; 655 BP.  
 XX AAV63638;  
 AC  
 XX 15-FEB-1999 (first entry)  
 DT  
 XX Contig 2153526 encoding a human desaturase enzyme.  
 DE  
 XX Fatty acid; desaturase; polyunsaturated fatty acid;  
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
 KW cholesterol level; endometriosis; premenstrual syndrome; human;  
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.  
 XX Homo sapiens.  
 OS  
 XX WO9846763-A1.  
 PN  
 XX 22-OCT-1998.  
 PD  
 XX 10-APR-1998; 98WO-US07126.  
 PF  
 XX 11-APR-1997; 97US-0834655.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA (CALJ ) CALGENE LLC.  
 XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
 PI Thurmond J;  
 PI WPI; 1998-594582/50.  
 DR P-PSDB; AAW84151.  
 XX





xx DE Contig 2153526 encoding a desaturase enzyme.

xx DE Fatty acid; desaturase; polyunsaturated fatty acid;

xx KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

xx KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

xx KW cholesterol level; endometriosis; premenstrual syndrome;

xx KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

xx KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

xx OS Homo sapiens.

xx KW WO9846765-A1.

xx PN 22-OCT-1998.

xx PD 10-APR-1998; 98WO-US07422.

xx PF 11-APR-1997; 97US-0833610.

xx PR (ABBO ) ABBOTT LAB.

xx PA (CALJ ) CALGENE LLC.

xx XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;

xx PI Thurmond J;

xx XX WPI; 1999-009334/01.

xx DR P-PSDB; AAW85130.

xx XX New nucleic acid encoding delta5 and other desaturase enzymes -

xx PT used in production of oils of increased arachidonic acid content,

xx PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics

xx XX Claim 86; Pages 107-108; 153pp; English.

xx XX The present sequence encodes a human desaturase enzyme. The enzyme

xx CC sequence is used in the methods of the invention. The specification

xx CC describes methods for desaturating a fatty acid and for producing a

xx CC desaturated fatty acid by expressing increased levels of a desaturase.

xx CC The enzyme can be used for desaturating fatty acids. The enzyme can be

xx CC used to produce polyunsaturated fatty acids, which can be used for

xx CC treating malnutrition, in pharmaceutical compositions, in cosmetics or

xx CC in animal feed. The polyunsaturated fatty acids can be used for treating

xx CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,

xx CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.

xx CC They can also be used to inhibit platelet aggregation, cause

xx CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel

xx CC wall smooth muscle and fibrous tissue, reduce or prevent

xx CC gastro-intestinal bleeding and other side effects caused by non-steroidal

xx CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual

xx CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after

xx CC viral infections, treat AIDS, multiple sclerosis, acute respiratory

xx CC syndrome, hypertension and inflammatory skin disorders.

xx XX Query Match 4.3%; Score 62.4; DB 20; Length 655;

xx XX Best Local Similarity 59.7%; Pred. No. 1.2e-06;

xx XX Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

xx XX Sequence 655 BP; 161 A; 181 C; 157 G; 156 T; 0 other;

QY 1123 CAAATCATGACCAACAAGATATGAGACCTGGAGATTCATTGCTGGCTTTGGGGAGGT 1182

DB 176 CAGCTCCAGGCCACATGCAATGCCAAGTCTGCTTCAATGCTGGTTCAGTGGACAC 235

QY 1183 CTTAACTATCAGATTGAGCACCACATCTTTCCCAACGATGCCAGACACAACTTGAACACT 1242

DB 236 CTCACCTTCAGAGTGGACACCATCTTTTCCCAACGATGCCAGACAACTTACCACAA 295

QY 1243 GTTATGCCACTTGTAAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTGA 1298

DB 296 GTGGCTCCCTGGTGCAGTCTCTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA 351

RESULT 15

AAA49934

ID AAA49934 standard; cDNA; 655 BP.

XX AC AAA49934;

XX AC AAA49934;

DT 10-OCT-2000 (first entry)

XX Human delta-5-desaturase-related contig 2153526.

XX Delta-5-desaturase; human; polyunsaturated fatty acid;

XX KW arachidonic acid; eicosapentaenoic acid; docosapentaenoic acid;

XX KW docosahexaenoic acid; nutrition; feedstuff; ss.

XX OS Homo sapiens.

XX WO2000040705-A2.

XX PN 13-JUL-2000.

XX PD 29-DEC-1999; 99WO-US31163.

XX PF 08-JAN-1999; 99US-0227613.

XX PR (ABBO ) ABBOTT LAB.

XX PA Mukerji P, Leonard AE, Huang Y, Parker-Barnes JM;

XX PI WPI; 2000-465975/40.

XX DR New polypeptide useful for preparation of nutritional supplements based

XX PT upon human DELTA5-desaturase, desaturates polyunsaturated fatty acids

XX PT at carbon 5 -

XX PS Example 1; Fig 3; 127pp; English.

XX XX The present sequence is that of contig 2153526, isolated from the

XX CC incyte Lifeseq database on the basis of homology to Mortierella

XX CC alpina delta-5-desaturase and delta-6-desaturase cDNA sequences.

XX CC A full-length cDNA (see AAA49932) for human delta-5-desaturase (see

XX CC AAY95445) was subsequently obtained. Delta-5-desaturase catalyzes

XX CC the conversion of dihomogamma-linolenic acid to arachidonic acid

XX CC and of 20:4n-3 to eicosapentaenoic acid. Recombinant enzyme,

XX CC expressed in prokaryotic or eukaryotic hosts using the isolated

XX CC human delta-5-desaturase cDNA, can be used in the production of

XX CC polyunsaturated fatty acids that may be added to nutritional,

XX CC veterinary and pharmaceutical compositions.

XX XX Query Match 4.3%; Score 62.4; DB 21; Length 655;

xx XX Best Local Similarity 59.7%; Pred. No. 1.2e-06;

xx XX Matches 105; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

xx XX Sequence 655 BP; 161 A; 181 C; 157 G; 156 T; 0 other;

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DB 176 CAGCTCCAGGCCACATGCAATGCCAAGTCTGCTTCAATGCTGGTTCAGTGGACAC 235

QY 1183 CTTAACTATCAGATTGAGCACCACATCTTTCCCAACGATGCCAGACACAACTTGAACACT 1242

DB 236 CTCACCTTCAGAGTGGACACCATCTTTTCCCAACGATGCCAGACAACTTACCACAA 295

QY 1243 GTTATGCCACTTGTAAAGGAGTTTGCAGCAGCAAAATGGTTTACCATACATGGTGA 1298

DB 296 GTGGCTCCCTGGTGCAGTCTCTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA 351

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Job time : 361.536 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_othr:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	641.4	43.9	643	13	BJ110522
3	633	43.3	649	13	BJ118587
C 4	618.4	42.3	665	13	BJ145121
C 5	617	42.2	661	13	BJ139786
C 6	617	42.2	662	13	BJ130343

C 7	616	42.2	660	13	BJ132419
C 8	616	42.2	661	13	BJ154980
C 9	616	42.2	674	13	BJ146307
C 10	615	42.1	656	13	BJ156149
C 11	615	42.1	659	13	BJ145290
C 12	614	42.0	658	13	BJ132385
C 13	613.4	42.0	660	13	BJ148253
C 14	613	42.0	677	13	BJ133013
C 15	611.4	41.9	656	13	BJ140489
C 16	611.4	41.8	659	13	BJ147839
C 17	611.2	41.8	660	9	AU213515
C 18	611	41.8	654	13	BJ140340
C 19	611	41.8	655	13	BJ138257
C 20	610.2	41.8	659	9	AU213354
21	607	41.5	629	13	BJ112369
22	606	41.5	637	13	BJ112079
23	605.8	41.5	609	9	AU201931
24	604.4	41.4	631	13	BJ126619
25	604	41.3	654	13	BJ132022
C 26	602.4	41.2	660	13	BJ146554
27	602	41.2	612	13	BJ102752
28	602	41.2	638	13	BJ119805
29	580	39.7	590	13	BJ127755
30	579.6	39.7	586	13	BJ174196
31	579	39.6	602	13	BJ104762
32	547	37.4	563	13	BJ120819
33	546.4	37.4	548	13	BJ120424
34	546	37.4	568	13	BJ112548
35	541	37.0	563	13	BJ112691
C 36	538.4	36.9	647	13	BJ141242
C 37	535.4	36.6	606	13	BJ140102
38	532.2	36.4	556	13	BJ118832
39	495	33.9	547	13	BJ105378
40	492	33.7	535	13	BJ104402
41	486.8	33.3	672	13	BJ104796
42	485.4	33.2	490	13	BJ117462
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#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
BJ149425 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1274d04 3', mRNA sequence.  
ACCESSION  
BJ149425  
VERSION  
EST.  
KEYWORDS  
EST.  
SOURCE  
Caenorhabditis elegans.  
ORGANISM  
Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae  
; Rhabditidae; Peleoderinae; Caenorhabditis.  
REFERENCE  
1 (bases 1 to 717)  
AUTHORS  
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
and Sugano,S.  
TITLE  
A complementary view of the C.elegans genome  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Tadasi Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1. 717  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"

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/clone="yk1274d04"
/clone_lib="unpublished oligo-capped cDNA library, C.
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/tissue_type="whole animal"
/dev_stage="L1"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      259 a 134 c 142 g 182 t
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Best Local Similarity 99.9%; Pred. No. 6.9e-157;
Matches 688; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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717 CGTGGGTATGACTCTATTCAGATGCGCAACATCTTCATTCGACATTCATCTTACCATTCC 658
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833 TCGCTCTCGTGGCTCTTTCAGTCAATCATTTTTTTTGTAGTCAGATGCCAATCATTTATT 892
   |||||||
657 TCGCTCTCGTGGCTCTTTCAGTCAATCATTTTTTTTGTAGTCAGATGCCAATCATTTATT 598
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893 ATGACTATTACAGAAATACATGCGATTATGACAGGTTGCTCTCTTTTGCACATGGGCTT 952
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597 ATGACTATTACAGAAATACATGCGATTATGACAGGTTGCTCTCTTTTGCACATGGGCTT 538
   |||||||
953 GGTCAATGGTCAATTTGATTTCTTACCCTGATTTGATGACAGGTTGCTCTCTTTTGCACATGGGCTT 1012
   |||||||
537 GGTCAATGGTCAATTTGATTTCTTACCCTGATTTGATGACAGGTTGCTCTCTTTTGCACATGGGCTT 478
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1013 TTTCTCATCTGTTGGAGGTTTCTGCTCTCTCATGTAGTACTTTCAATCATTTATTCAG 1072
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477 TTTCTCATCTGTTGGAGGTTTCTGCTCTCTCATGTAGTACTTTCAATCATTTATTCAG 418
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   |||||||
1133 CCACAGAAATATGACACCTGGAGATTTCAATTCAGCTGGCTTTGGGAGGCTTAACTATC 1192
   |||||||
357 CCACAGAAATATGACACCTGGAGATTTCAATTCAGCTGGCTTTGGGAGGCTTAACTATC 298
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1193 AGATTGAGCACCATTCTTTCCCAACGATGCGACACACAACTTGAACACTGTTATGCGAC 1252
   |||||||
297 AGATTGAGCACCATTCTTTCCCAACGATGCGACACACAACTTGAACACTGTTATGCGAC 238
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1253 TTGTTAAGGATTTGCGAGCAGCAAAATGGTTTACCATACATATGCTGCGAGCATTTTTCACAG 1312
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177 GATTCCTGGCTTGAATTTGACCAATTCGGAATATGCAAAATGCTGCTAAATGACTA 118
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1373 AAAAGATTTGCTAGATTACCATTAATTAATCAATTTTATTTTCATGTTCTATTCGTGTT 1432
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117 AAAAGATTTGCTAGATTACCATTAATTAATCAATTTTATTTTCATGTTCTATTCGTGTT 58
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1433 TTAATATTTTCCAAATTTTACCCTATTTC 1461
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57 TTAATATTTTCCAAATTTTACCCTATTTC 29
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RESULT 2
BJ110522
LOCUS
DEFINITION
Caenorhabditis elegans cDNA clone yk113h06 5', mRNA sequence.
ACCESSION
BJ110522

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VERSION          BJ110522.1  GI:18270559
KEYWORDS
SOURCE           Caenorhabditis elegans.
ORGANISM         Caenorhabditis elegans
REFERENCE        1 (bases 1 to 643)
AUTHORS          Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE            A complementary view of the C.elegans genome
COMMENT          Unpublished (2002)
                  Contact: Tadasu Shin-i
                  Center For Genetic Resource Information
                  National Institute of Genetics
                  1111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshini@genes.nig.ac.jp.
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        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
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        cDNAs were cloned into pPC86"
BASE COUNT      212 a 126 c 122 g 183 t
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Matches 642; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1  AGACAAGAGATGAGCAGCATCTTCTTCAATTAATAATGATGAAATGCTGTCAAATTGACGA 60
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114 TGCTGTCTCTGAGATCAGATCCAGTGGTGTAGTSCAAATTAACCTATAAAATATATGATGC 173
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61 TGCTGTCTCTGAGATCAGATCCAGTGGTGTAGTSCAAATTAACCTATAAAATATATGATGC 120
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174 CACTACCGTATTCCACACATTCATCTGTTCTAAAGAAGGATCAATGGCTGACAGA 233
   |||||||
121 CACTACCGTATTCCACACATTCATCTGTTCTAAAGAAGGATCAATGGCTGACAGA 180
   |||||||
234 ATTGAAAAGAGTGGCCCTACACAGAACACAGAGATCCAGATATTAAGGATGACCCAAT 293
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354 AATAAATAAAGTTTCACTGATCTGATACGATCGGAGTTCGTCGAGAACGATATGATGG 413
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414 ATCTCCTTTGTTCTTACATTTAGAAAATCTTGAACATCTTCAAAATCTTTTTCGATT 473
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361 ATCTCCTTTGTTCTTACATTTAGAAAATCTTGAACATCTTCAAAATCTTTTTCGATT 420
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DEFINITION BJ130343 unpublished oligo-capped cDNA library, C. elegans L1 stage
ACCESSION BJ130343
VERSION BJ130343.1 GI:18290500
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SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS : Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 662)
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
BASE COUNT 242 a 122 c 126 g 171 t 1 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.8e-140;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 542 AATTGTATTTCTACCCGATTTGGTCAACTAGATAATGTCTCTCTCTCTCTCTCTCTCTCTCTCT 483
QY 1025 TTGGAGGTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1084
DB 482 TTGGAGGTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 423
QY 1085 CATTTGAGCTGCAACATCATGTCAATTTAGCTTGTCTTCAATCATGACCAACAAGATA 1144
DB 422 CATTTGAGCTGCAACATCATGTCAATTTAGCTTGTCTTCAATCATGACCAACAAGATA 363
QY 1145 TGAGACCTGGAAGATTCAATTCAGTGGCTTTGGGGAGTCTTAACATATCAGATTGAGCACC 1204
DB 362 TGAGACCTGGAAGATTCAATTCAGTGGCTTTGGGGAGTCTTAACATATCAGATTGAGCACC 303
QY 1205 ATCTTTTCCCAACGATGCCACGACACACTTTGAACACTGTTATGCCACTTGTGTAAGGAGT 1264
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DEFINITION BJ132419 unpublished oligo-capped cDNA library, C. elegans L1 stage
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VERSION BJ132419.1 GI:18292576
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SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS : Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 660)
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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            /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"
BASE COUNT 242 a 121 c 126 g 171 t
ORIGIN
Query Match 42.2%; Score 616; DB 13; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.7e-139;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 906 AAATACTGCGATTATGACACAGGTGGTCTCTCTTTCGACTGGGCTTGGTCATTTGGGTCA 965
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/note="The AD-wmcdna library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

BASE COUNT 242 a 119 c 125 g 171 t 1 others  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.2e-139;

Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 848 TTCTTCAGTCATCATTTTGTAGTCAGATGCCAATCAATTAATGACTATTACAGAA 907
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Db 358 GACCTGGAGATTCATTTAGCTAGCTTTGGGAGGCTTAACTATCATGATGAGCACCATC 299
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Db 58 TTTTACCCTATTCC 45

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# RESULT 13 BJ148253/c

LOCUS BJ148253 660 bp mRNA linear EST 24-JAN-2002  
DEFINITION BJ148253 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1260f09 3', mRNA sequence.

ACCESSION BJ148253  
VERSION BJ148253.1 GI:18316238  
KEYWORDS EST.

SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea  
; Rhabditidae; Pelodierinae; Caenorhabditis.

AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
and Sugano,S.

TITLE A complementary view of the C.elegans genome

## JOURNAL COMMENT

Unpublished (2002)  
Contact: Tadasi Shin-I  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.

## FEATURES source

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/sex="hermaphrodite"  
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/dev\_stage="L1"  
/note="The AD-wmcdna library was generated with poly(A)+  
RNA isolated from both hermaphrodite and male N2 worms of  
all larval stages, embryos, adults and dauers and the  
subsequent generation of cDNAs by poly(A) priming. The  
cDNAs were cloned into pPC86"

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ORIGIN

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Best Local Similarity 99.7%; Pred. No. 7.4e-139;

Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      60 AATTTTACCTATTCC 45

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BJ133013
VERSION  BJ133013.1 GI:18293170
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SOURCE   Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
          ; Rhabditidae; Peloderinae; Caenorhabditis.
          1 (bases 1 to 677)
REFERENCE Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
          and Sugano,S.
          A complementary view of the C.elegans genome
          Unpublished (2002)
          Contact: Tadasu Shin-I
          Center For Genetic Resource Information
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
          Email: tshini@genes.nig.ac.jp.
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              /strain="N2"
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              elegans L1 stage"
              /sex="hermaphrodite"
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              /dev_stage="L1"
              /note="The AD-wrmcDNA library was generated with poly(A)+
              RNA isolated from both hermaphrodite and male N2 worms of
              all larval stages, embryos, adults and dauers and the
              subsequent generation of cDNAs by poly(A) priming. The
              cDNAs were cloned into pPC86"
BASE COUNT  246 a 125 c 126 g 179 t 1 others
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Best Local Similarity 100.0%; Pred. No. 9.2e-139;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION
BJ140489
VERSION  BJ140489.1 GI:18300655
KEYWORDS
EST.
SOURCE   Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
          ; Rhabditidae; Peloderinae; Caenorhabditis.
          1 (bases 1 to 656)
REFERENCE Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
          and Sugano,S.
          A complementary view of the C.elegans genome
          Unpublished (2002)
          Contact: Tadasu Shin-I
          Center For Genetic Resource Information
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
          Email: tshini@genes.nig.ac.jp.
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              RNA isolated from both hermaphrodite and male N2 worms of
              all larval stages, embryos, adults and dauers and the
              subsequent generation of cDNAs by poly(A) priming. The
              cDNAs were cloned into pPC86"
BASE COUNT  240 a 120 c 125 g 171 t
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Best Local Similarity 100.0%; Pred. No. 1.6e-138;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1030 GGTTCCTCCTCTCATCTAGTTACTTTCAATCATATATCAGTGAGAGTTTGCATTG 1089
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QY 1090 ACCTCGAATCATATGTCRAATACGTTCTCTTCAATCATGACACACAGAAATATGAGA 1149
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QY 1150 CCTGGAAGATTCAATTGACTGGCTTTGGGGAGGTCTTAACTATCAGATTGAGCACCACATCTT 1209
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QY 1210 TTCCCAACGATGCCAGACACAACTTGAACACTGTTATGCCACTTGTAAAGGAGTTTGA 1269
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QY 1270 GCAGCAAAATGGTTTACCATACATGGTCGACGATTATTTACAGGATTCTGGCTTGAATT 1329
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 16:49:50 ; Search time 16.4603 Seconds  
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Total number of hits satisfying chosen parameters: 262574

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	629	25.8	458	4	US-09-439-261-10
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8	629	25.8	458	4	US-09-227-613-11
9	629	25.8	458	4	US-09-227-613-41
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19	408.5	16.8	432	4	US-09-227-613-9
20	408.5	16.8	465	4	US-09-439-261-40
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28	402.5	16.5	444	4	US-09-227-613-12	Sequence 12, Appl
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31	396	16.3	444	4	US-09-439-261-43	Sequence 43, Appl
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33	387	15.9	452	4	US-08-934-254-27	Sequence 27, Appl
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42	284.5	11.7	87	2	US-08-834-655-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KURTZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMUND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,655  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RAE-VENTER, BARBARA  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CGNE.124.0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 328-4400  
; TELEFAX: (650) 328-4477  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-834-655-2

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Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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## RESULT 2

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: Patent No. 6075183
: GENERAL INFORMATION:
: APPLICANT: KNUTZON, DEBORAH
: APPLICANT: MURKERT, PRADIP
: APPLICANT: HUANG, YUNG-SHENG
: APPLICANT: THURMOND, JENNIFER
: APPLICANT: CHAUDHARY, SUNITA
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
: TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
: STREET: 2001 FERRY BUILDING
: CITY: SAN FRANCISCO
: STATE: CA
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/834,033A
: FILING DATE: 11-APR-1997
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: WARD, MICHAEL R.
: REGISTRATION NUMBER: 38,651
: REFERENCE/DOCKET NUMBER: CGAB-300.USA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 433-4150
: TELEFAX: (415) 433-8716
: TELEX: N/A
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 457 amino acids
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match 25,88; Score 629; DB 3; Length 457;
Best Local Similarity 33.08; Pred. No. 1.1e-54;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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QY 64 ELKKECTOPEIPDIDKDDPIKIGIDDDVNMGTFNISEKRSQAQINKSFDTDLRMVRAEGLMD 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 LANFYVGDIIDSDRIDKDDF-----AAEVRK-----LRTLQSLGYD 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 GSPLFYIRKI-----LETITILFAFYLOYHTY-YLPSSAILMGVAMQOLGWLHIEFAHQ 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 SSKAYIAFKYSFNLICINGLSTVIYAKWGOTSTLANVLSAALLGLFWQCGWLHDFLHQ 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 178 LFNRYNDLASFYVGNFLOGSSGKQEHNVHHAATNVVGRDGLDLPFYATVAEHL 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 VFODRFWGDLFGLAGVCGGFSSSWKDKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLQSIIFV-----SQ 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 LEMFSDVPDELTRMWSRFMYLNTWFFYFPLSFARLSWCLQSLFVLPNGQAHKPSGAR 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 MPYHYDYRYNTAIYEQVGLSLHWASLGOLY-FLPDWSTRIMFVLSHLVGGFLLSHV 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 VP-----ISLVEQLSLAMHTWYLATMFLFIKDPVNMVFLVLSQVCGNLLAIVF 348
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 TENHYSVEKFSALSSNMSYACQIMTTRNMRPGREFIDWLGGIYQIEHHLFPTMPRH 397
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 349 SLNHGMPVISKEAAMDVDFTKOITGRDVHPLGFANWFTGGLNYQIEHHLFPTMPRH 408
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 398 LNTVMPLVKEFAAANGLPYVMDYFTGFWLEIEOFRNIANVAALTK 444
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 409 FSKIQPAVETLCKKYNRYHTGTGIEGTAEVFSRLNEVSKAASKMGK 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-09-363-574-2
: Sequence 2, Application US/09363574
: Patent No. 6136574
: GENERAL INFORMATION:
: APPLICANT: KNUTZON, DEBORAH
: APPLICANT: MURKERT, PRADIP
: APPLICANT: HUANG, YUNG-SHENG
: APPLICANT: THURMOND, JENNIFER
: APPLICANT: CHAUDHARY, SUNITA
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
: TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
: STREET: 2001 FERRY BUILDING
: CITY: SAN FRANCISCO
: STATE: CA
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/363,574
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
```

NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-202 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 457 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-363-574-2

Query Match 25.8%; Score 629; DB 4; Length 457;  
Best Local Similarity 33.0%; Pred. No. 1.le-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 ROEHEPPFIKIDGKCQIDDVLRSHPGGSAITTYKNMDATTVFHTGSKRAYQWLT 63  
DB 25 KKDAEAPFLMIIDNKVYDVREFV-PDHPGGSVILTHVGKDGTDVDFTFH---PEA-AWET 79  
QY 64 ELKKECPTQEPPIKDDPIKIDGIDVNMGTFFNISEKRSQAQINKSFTDLRMVRAEGLMD 123  
DB 80 LANFYVGDDIDESDRDINKDDF-----AAEVRK-----LRTLFSLSGYD 118  
QY 124 GSPFLFYIRKI-----LETIFTILFAFYLOVHTY-YLPSAILMGVAMQQLGLIHEFAHHQ 177  
DB 119 SSKAYYAFKVSFNLCTGLSTVIVAKWGQSTLANVLSAALLGLFWQCGWLADFLHHQ 178  
QY 178 LFNRYNDLASFYVGNFLOGSSGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
DB 179 VFQDRFWGDLFGAFLGCVCGQSSWWKDKHNTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWWMTLFRWQHVHTF--MLPFLRLSLWLLQSIIFV-----SQ 278  
DB 238 LEMFSDVPDEELTRMMSRFVNLQNTWFFPILSFARLSWCLQSLFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHWANSLGOLY-FLPDWSTRIMFFLVSHLVGGLLSHVY 337  
DB 298 VP-----ISLVEQLSLAMHWTWYLATMFLFKDPVNMVLYFLVSQAVCNLLAIYF 348  
QY 338 TFNHYVEKFASSNTMSNYACIQIMTRNMRGRFIDMLWGLNLYQIEHLLFTPMRHN 397  
DB 349 SLNHGMPVISKEEAVIDMDFETKQIITGRDVHPGLEFANFTGGLNYQIEHLLFPSMPRHN 408  
QY 398 LNTVMPLVKFEAAANGLPYVDDYFTGFWLEIEQFRNIANVAALTK 444  
DB 409 FSKIQPAVETLCKKNYRVHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 4  
US-09-363-526-2  
Sequence 2, Application US/09363526  
Patent No. 6410288  
GENERAL INFORMATION:  
APPLICANT: KNUZON, DEBORAH  
APPLICANT: MURKERJI, PRADIP  
APPLICANT: HUANG, YUNG-SHENG  
APPLICANT: THORMOND, JENNIFER  
APPLICANT: CHAUDHARY, SUNITA  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.  
STREET: 2001 FERRY BUILDING  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 457 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-363-526-2

Query Match 25.8%; Score 629; DB 4; Length 457;  
Best Local Similarity 33.0%; Pred. No. 1.le-54;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 ROEHEPPFIKIDGKCQIDDVLRSHPGGSAITTYKNMDATTVFHTGSKRAYQWLT 63  
DB 25 KKDAEAPFLMIIDNKVYDVREFV-PDHPGGSVILTHVGKDGTDVDFTFH---PEA-AWET 79  
QY 64 ELKKECPTQEPPIKDDPIKIDGIDVNMGTFFNISEKRSQAQINKSFTDLRMVRAEGLMD 123  
DB 80 LANFYVGDDIDESDRDINKDDF-----AAEVRK-----LRTLFSLSGYD 118  
QY 124 GSPFLFYIRKI-----LETIFTILFAFYLOVHTY-YLPSAILMGVAMQQLGLIHEFAHHQ 177  
DB 119 SSKAYYAFKVSFNLCTGLSTVIVAKWGQSTLANVLSAALLGLFWQCGWLADFLHHQ 178  
QY 178 LFNRYNDLASFYVGNFLOGSSGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
DB 179 VFQDRFWGDLFGAFLGCVCGQSSWWKDKHNTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWWMTLFRWQHVHTF--MLPFLRLSLWLLQSIIFV-----SQ 278  
DB 238 LEMFSDVPDEELTRMMSRFVNLQNTWFFPILSFARLSWCLQSLFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHWANSLGOLY-FLPDWSTRIMFFLVSHLVGGLLSHVY 337  
DB 298 VP-----ISLVEQLSLAMHWTWYLATMFLFKDPVNMVLYFLVSQAVCNLLAIYF 348  
QY 338 TFNHYVEKFASSNTMSNYACIQIMTRNMRGRFIDMLWGLNLYQIEHLLFTPMRHN 397  
DB 349 SLNHGMPVISKEEAVIDMDFETKQIITGRDVHPGLEFANFTGGLNYQIEHLLFPSMPRHN 408  
QY 398 LNTVMPLVKFEAAANGLPYVDDYFTGFWLEIEQFRNIANVAALTK 444  
DB 409 FSKIQPAVETLCKKNYRVHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 5  
US-09-330-235-18  
Sequence 18, Application US/09330235  
Patent No. 6459018  
GENERAL INFORMATION:  
APPLICANT: Knutzon, Debbie  
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
FILE REFERENCE: MOCO.156.0005  
CURRENT APPLICATION NUMBER: US/09/330,235  
CURRENT FILING DATE: 1999-06-10





```
Query Match          25.8%; Score 629; DB 4; Length 458;
Best Local Similarity 33.0%; Pred. No. 1.1e-54;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 REOEHEPFFIKIDGKCQIDDAVLRSHPGGSAITTYKKNMDATTVFHTGSKAEYQWLT 63
DB 25 KKDAEAPFLMIIDNKVYDREVF-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
QY 64 ELKKECTQEPDIPKDDPKIGDIDVNMGTFNISEKRSQAQINKSFIDLRMRVRAEGLMD 123
DB 80 LANFYVGDDIDESDRDIKNDFF-----AAEVRK-----LRTLFSQSLGYD 118

QY 124 GSPFLFYIRKI-----LETITILFAFYLOHYTY-YLPSSAILMGVAMQOLGWLHIEFAHQ 177
DB 119 SSKAYYAFKVSFNLCTWGLSTVIVAKWGQSTLANVLSAALLGLFWQCCGWLADHFLHQ 178
QY 178 LFKNRYNDLASFYVGNFLQGSFGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237
DB 179 VFQDRFWGDLFGAFLGVCQGSFSSWKKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
QY 238 NNYSDQ-----SWVMTLFRWQHVVHTF--MLPFLRLSWLQSIIFV-----SQ 278
DB 238 LEMFSDVPDEELTRMWSRFLVNTQWTFYFPILSFARLSWCLQSIILFVLPNGOAHKPSGAR 297
QY 279 MPTHYDYRYNTAIYEOVGLSLHWANSLGOLY-FLPDWSTRIMEFLVSHLVGGLSHV 337
DB 298 VP-----ISLVEQLSLAMHWYLTATMFLFIKDPVNMVLYFLVSQAVCGNLLAIVF 348
QY 338 TFNHYSVKEFALSSNMSNYACLIQIMTRNMRPGRFIDWLWGLNLYQIEHHLFPTMPRH 397
DB 349 SLNHNMGMPVISKEEAVDMDEFTKQIITGRDVHFGCLFANWFTGGLNYQIEHHLFPTMPRH 408
QY 398 LNTVMPLVKEFAAANGPLVMYDDYFTGFWELEIQFNRNIANVAKLTK 444
DB 409 FSKIQPAVETLCKKNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 9
US-09-227-613-41
; Sequence 41, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
; OTHER INFORMATION: Xaa at position 458 is unknown or other.
US-09-227-613-41

Query Match          25.8%; Score 629; DB 4; Length 458;
Best Local Similarity 33.0%; Pred. No. 1.1e-54;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 REOEHEPFFIKIDGKCQIDDAVLRSHPGGSAITTYKKNMDATTVFHTGSKAEYQWLT 63
DB 25 KKDAEAPFLMIIDNKVYDREVF-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
QY 64 ELKKECTQEPDIPKDDPKIGDIDVNMGTFNISEKRSQAQINKSFIDLRMRVRAEGLMD 123
DB 80 LANFYVGDDIDESDRDIKNDFF-----AAEVRK-----LRTLFSQSLGYD 118

QY 124 GSPFLFYIRKI-----LETITILFAFYLOHYTY-YLPSSAILMGVAMQOLGWLHIEFAHQ 177
DB 119 SSKAYYAFKVSFNLCTWGLSTVIVAKWGQSTLANVLSAALLGLFWQCCGWLADHFLHQ 178
QY 178 LFKNRYNDLASFYVGNFLQGSFGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237
DB 179 VFQDRFWGDLFGAFLGVCQGSFSSWKKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
QY 238 NNYSDQ-----SWVMTLFRWQHVVHTF--MLPFLRLSWLQSIIFV-----SQ 278
DB 238 LEMFSDVPDEELTRMWSRFLVNTQWTFYFPILSFARLSWCLQSIILFVLPNGOAHKPSGAR 297
QY 279 MPTHYDYRYNTAIYEOVGLSLHWANSLGOLY-FLPDWSTRIMEFLVSHLVGGLSHV 337
DB 298 VP-----ISLVEQLSLAMHWYLTATMFLFIKDPVNMVLYFLVSQAVCGNLLAIVF 348
QY 338 TFNHYSVKEFALSSNMSNYACLIQIMTRNMRPGRFIDWLWGLNLYQIEHHLFPTMPRH 397
DB 349 SLNHNMGMPVISKEEAVDMDEFTKQIITGRDVHFGCLFANWFTGGLNYQIEHHLFPTMPRH 408
QY 398 LNTVMPLVKEFAAANGPLVMYDDYFTGFWELEIQFNRNIANVAKLTK 444
DB 409 FSKIQPAVETLCKKNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 8
US-09-227-613-11
; Sequence 11, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
; OTHER INFORMATION: Xaa at position 458 is unknown or other.
US-09-227-613-11

Query Match          25.8%; Score 629; DB 4; Length 458;
Best Local Similarity 33.0%; Pred. No. 1.1e-54;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY 4 REOEHEPFFIKIDGKCQIDDAVLRSHPGGSAITTYKKNMDATTVFHTGSKAEYQWLT 63
DB 25 KKDAEAPFLMIIDNKVYDREVF-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
QY 64 ELKKECTQEPDIPKDDPKIGDIDVNMGTFNISEKRSQAQINKSFIDLRMRVRAEGLMD 123
DB 80 LANFYVGDDIDESDRDIKNDFF-----AAEVRK-----LRTLFSQSLGYD 118

QY 124 GSPFLFYIRKI-----LETITILFAFYLOHYTY-YLPSSAILMGVAMQOLGWLHIEFAHQ 177
DB 119 SSKAYYAFKVSFNLCTWGLSTVIVAKWGQSTLANVLSAALLGLFWQCCGWLADHFLHQ 178
QY 178 LFKNRYNDLASFYVGNFLQGSFGGKQHNHHAATNVVGRDGLDLVPFYATVAEHL 237
DB 179 VFQDRFWGDLFGAFLGVCQGSFSSWKKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237
QY 238 NNYSDQ-----SWVMTLFRWQHVVHTF--MLPFLRLSWLQSIIFV-----SQ 278
DB 238 LEMFSDVPDEELTRMWSRFLVNTQWTFYFPILSFARLSWCLQSIILFVLPNGOAHKPSGAR 297
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;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 355 amino acids  
 ;; TYPE: amino acid  
 ;; STRANDEDNESS: not relevant  
 ;; TOPOLOGY: linear  
 ;; MOLECULE TYPE: peptide  
 US-08-834-033A-6

Query Match 22.8%; Score 555; DB 3; Length 355;  
 Best Local Similarity 34.5%; Pred. No. 2e-47;  
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;  
 QY 112 LRMVRAGLMDGSPFLVIRKI-----LETITILFAFYLOYHTY-YLPSSAILMGVAWQQ 165  
 DB 5 LRTLFQSLGYDSSKAYAFKVSFNLGICWGLSTVIVAKWGOTSTLANVLSAALLGLFWQQ 64  
 QY 166 LGWLIHEFAHQLFKNRYNDLASFYVGNFQSGSGGWKEQHNHHAAATNVVGRDGLD 225  
 DB 65 CGWLADFLHHQVQDFRFGDLFGAFLGGVCGGFSWKKDKHNTTHAAAPNVHGEDPDID 124  
 QY 226 LVPEYATVAEHLNYSQD-----SWVMTLFRQHVHTF--MLPFLRLSWLQSLIFV- 276  
 DB 125 THPL-LTWSEHALEMFSDVPDEELTRMWSRFVNLQNTWFFPILSFARLSWCLQSLIFVL 183  
 QY 277 -----SOMPTHYDYRNTAIYEQVGLSLHAWSLGOLY-FLPDWSTRIMFVLVS 325  
 DB 184 PNGAHKPSGARVP-----ISLVEQLSLAHMTWYLATMFLFIKDPVNNMLVYFLVS 234  
 QY 326 HLVGFLSHVVTNHYSVKFASSNIMSNYACLIQIMTRNMRPGREIDWLWGOLNYOI 385  
 DB 235 QAVCGNLLAIVFSLNHNMGVPSKEEAVDMDFFTKQIITGRDVHGLFANFTGSLNYOI 294  
 QY 386 EHHLPMPRNLNTVMPLVKEFAAANGLPYVDDYFTGFWELEIQFRNIANVAKLTK 444  
 DB 295 EHHLPSPMRHNSKIOPAVETLCKKNVRYHTTGMIETGAEVFSRLNEVSKAASKMGK 353

## RESULT 14

US-09-363-574-5  
 ; Sequence 5, Application US/09363574  
 ; Patent No. 6136574

## GENERAL INFORMATION:

;; APPLICANT: KNUTZON, DEBORAH  
 ;; APPLICANT: MURKERJI, PRADIP  
 ;; APPLICANT: HUANG, YUNG-SHENG  
 ;; APPLICANT: THURMOND, JENNIFER  
 ;; APPLICANT: CHAUDHARY, SUNITA

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

;; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

;; NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

;; STREET: 2001 FERRY BUILDING

;; CITY: SAN FRANCISCO

;; STATE: CA

;; COUNTRY: USA

;; ZIP: 94111

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent in Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/363.574

;; FILING DATE:

;; CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: WARD, MICHAEL R.

;; REGISTRATION NUMBER: 38,651

;; REFERENCE/DOCKET NUMBER: CGAB-202 USA

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 433-4150

;; TELEFAX: (415) 433-8716

;; TELEX: N/A  
 ;; INFORMATION FOR SEQ ID NO: 5:  
 ;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 355 amino acids  
 ;; TYPE: amino acid  
 ;; STRANDEDNESS: not relevant  
 ;; TOPOLOGY: linear  
 ;; MOLECULE TYPE: peptide  
 US-09-363-574-5

Query Match 22.8%; Score 555; DB 4; Length 355;  
 Best Local Similarity 34.5%; Pred. No. 2e-47;  
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;  
 QY 112 LRMVRAGLMDGSPFLVIRKI-----LETITILFAFYLOYHTY-YLPSSAILMGVAWQQ 165  
 DB 5 LRTLFQSLGYDSSKAYAFKVSFNLGICWGLSTVIVAKWGOTSTLANVLSAALLGLFWQQ 64  
 QY 166 LGWLIHEFAHQLFKNRYNDLASFYVGNFQSGSGGWKEQHNHHAAATNVVGRDGLD 225  
 DB 65 CGWLADFLHHQVQDFRFGDLFGAFLGGVCGGFSWKKDKHNTTHAAAPNVHGEDPDID 124  
 QY 226 LVPEYATVAEHLNYSQD-----SWVMTLFRQHVHTF--MLPFLRLSWLQSLIFV- 276  
 DB 125 THPL-LTWSEHALEMFSDVPDEELTRMWSRFVNLQNTWFFPILSFARLSWCLQSLIFVL 183  
 QY 277 -----SOMPTHYDYRNTAIYEQVGLSLHAWSLGOLY-FLPDWSTRIMFVLVS 325  
 DB 184 PNGAHKPSGARVP-----ISLVEQLSLAHMTWYLATMFLFIKDPVNNMLVYFLVS 234  
 QY 326 HLVGFLSHVVTNHYSVKFASSNIMSNYACLIQIMTRNMRPGREIDWLWGOLNYOI 385  
 DB 235 QAVCGNLLAIVFSLNHNMGVPSKEEAVDMDFFTKQIITGRDVHGLFANFTGSLNYOI 294  
 QY 386 EHHLPMPRNLNTVMPLVKEFAAANGLPYVDDYFTGFWELEIQFRNIANVAKLTK 444  
 DB 295 EHHLPSPMRHNSKIOPAVETLCKKNVRYHTTGMIETGAEVFSRLNEVSKAASKMGK 353

## RESULT 15

US-09-363-526-5  
 ; Sequence 5, Application US/09363526  
 ; Patent No. 6410288

## GENERAL INFORMATION:

;; APPLICANT: KNUTZON, DEBORAH  
 ;; APPLICANT: MURKERJI, PRADIP  
 ;; APPLICANT: HUANG, YUNG-SHENG  
 ;; APPLICANT: THURMOND, JENNIFER  
 ;; APPLICANT: CHAUDHARY, SUNITA

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

;; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

;; NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

;; STREET: 2001 FERRY BUILDING

;; CITY: SAN FRANCISCO

;; STATE: CA

;; COUNTRY: USA

;; ZIP: 94111

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent in Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/363.526

;; FILING DATE:

;; CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: WARD, MICHAEL R.

;; REGISTRATION NUMBER: 38,651

;; REFERENCE/DOCKET NUMBER: CGAB-201 USA

;; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150  
 TELEFAX: (415) 433-8716  
 TELEX: N/A  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 355 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-363-526-5

Query Match 22.8%; Score 555; DB 4; Length 355;  
 Best Local Similarity 34.5%; Pred. No. 2e-47;  
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;

QY	112	LRNRVRAEGLMDGSPLEFYIRKI-----LETIFTILFAFYLYQYHTY-YLPSAILMGVAMQO	165
Db	5	LRTLFOSLGYDSSKAYAFKVSFNLCIWLSTVIVAKWGQTSTLANVLSAALLGLFWQO	64
QY	166	LGWLIHEFAHQLFKHRYNDLASYPVGNFLQGFSSGGHKEQHNVHHAATNVVGRDGLD	225
Db	65	CGMLAHDFLHQVDFORFGDLFGAFLGVCQGFSSSWKDKHNTTHAAPNVHGEDPDID	124
QY	226	LVPEYATVAEHLNNYSQD-----SKVMTLFRWQVHWTFF--MLPELRLSWLLQSIIFV-	276
Db	125	THPL-LTWSEHALEMFSVDPDEELTRMSRFMYLNTWTFYFPLSFARLSWCISILFVL	183
QY	277	-----SQMPTHYYDYRYNTAIYEQVGLSLHWASLGQLY-FLPDWSTRIMFFLVS	325
Db	184	PNGQAHKPSGARVP-----ISLVEQLSLAHHTWYLAHWFELFKDPVNMVLYFLVS	234
QY	326	HLVGGFLLSHVTFNHYSEKFPALSSNIMSNYACLIQIMTRNMRPGRFIDMLMGGLNYQI	385
Db	235	QAVCGNLLAIVFSLNHNGMPVISKEAVDMDFTKQIITGRDVPGLFANWFTGGLNYQI	294
QY	386	EHLLEPTMPRHNLNTVMPLVKPEFAAANGPLPYVDDYFTGFWEIEQFRNIANYAAKLT	444
Db	295	EHLFPSPMRHNSFKIQPAVETLCKKYNRYHTTGMEGTAEVFSRLNEVSKAASRMKG	353

Search completed: July 2, 2003, 19:28:43  
 Job time: 18.4603 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 12:59:11 ; Search time 3361.32 Seconds  
(without alignments)  
11039.134 Million cell updates/sec

Title: US-09-857-583-3  
Perfect score: 1275  
Sequence: 1 atttttttcgaatgaagt.....gcggggaagctctataagg 1275

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*  
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16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
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32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rtd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1275	100.0	1275	8	AF139720	AF139720 Euglena g
2	121.6	9.5	1374	8	AF306634	AF306634 Mortierel
3	121.6	9.5	1617	6	AR080598	AR080598 Sequence
4	121.6	9.5	1617	6	AR098439	AR098439 Sequence
5	121.6	9.5	1617	6	AR136018	AR136018 Sequence
6	121.6	9.5	1617	8	AF110510	AF110510 Mortierel
7	118.4	9.3	1374	8	AF307940	AF307940 Mortierel
8	118.4	9.3	1374	8	AF465281	AF465281 Mortierel
9	118.4	9.3	1374	8	AF465282	AF465282 Mortierel
10	118.4	9.3	1374	8	AF465283	AF465283 Mortierel
11	113.6	8.9	1590	8	AB020032	AB020032 Mortierel
12	112.8	8.8	1463	3	AF031477	AF031477 Caenorhab
13	112.8	8.8	1463	6	AX003603	AX003603 Sequence
14	108.8	8.5	1344	3	AF078796	AF078796 Caenorhab
15	108.8	8.5	1344	6	AX020906	AX020906 Sequence
16	108.8	8.5	1461	3	AF114440	AF114440 Caenorhab
17	107.4	8.4	1380	6	AX467717	AX467717 Sequence
18	107.4	8.4	1380	8	AF419296	AF419296 Pythium i
19	103.2	8.1	1071	8	AF307941	AF307941 Mortierel
20	103.2	8.1	1644	8	AF307942	AF307942 Mortierel
21	79.4	6.2	1546	8	AB052086	AB052086 Mucor cir
22	71.6	5.6	1467	6	AX058832	AX058832 Sequence
23	71.6	5.6	2040	6	AX058830	AX058830 Sequence
24	71.6	5.6	2040	8	CPU250734	CPU250734 Ceratodon
25	71.2	5.6	96312	2	AP005554	AP005554 Oryza sat
26	70	5.5	44274	1	SCHE3	AL442629 Streptomy
27	69.8	5.5	1594	6	AX007239	AX007239 Sequence
28	69.8	5.5	1610	8	BNJ4160	AJ224160 Brassica
29	69.6	5.5	1788	8	AF031194	AF031194 Triticum
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31	68.6	5.4	1434	6	AX481942	AX481942 Sequence
32	68.6	5.4	1669	8	AY082393	AY082393 Phaeodact
33	60.8	4.8	1591	8	HACYTB5RN	X87143 Helianthus
34	60.8	4.8	1606	6	AX007273	AX007273 Sequence
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36	56.4	4.4	2160	6	AX058840	AX058840 Sequence
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39	56	4.4	1678	6	AX007241	AX007241 Sequence
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ALIGNMENTS

RESULT 1  
AF139720  
LOCUS AF139720 1275 bp mRNA linear PLN 29-JUL-1999  
DEFINITION Euglena gracilis delta8 fatty acid desaturase (efd1) mRNA, complete cds.  
ACCESSION AF139720  
VERSION AF139720.1 GI:5639723  
KEYWORDS  
SOURCE Euglena gracilis.  
ORGANISM Euglena gracilis  
Eukaryota; Euklenozoa; Euglenida; Euglenales; Euglena.  
REFERENCE 1 (bases 1 to 1275)  
AUTHORS Wallis J.G. and Browse J.  
TITLE The Delta8-desaturase of Euglena gracilis: an alternate pathway for synthesis of 20-carbon polyunsaturated fatty acids





University, 94 Weijin Road, Tianjin 300071, People's Republic of China

FEATURES  
source  
CDS

Location/Qualifiers  
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GLFWQCQGLAHDFLHQVDFQDFWDLFGALGCVGCFSSWMKDKRHHAAAPNV  
HGEDPDITHLPTWSEHALEFSDVDPBELTRMNSREWLVNQTWYFPIILSFARLW  
CLOSLVLPNGQAHKPSGARVSIISLQLSLAHWTWYLAITMELFKDPVNMWYEL  
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BASE COUNT 260 a 393 c 359 g 362 t

Query Match 9.5%; Score 121.6; DB 8; Length 1374;  
Best Local Similarity 49.3%; Pred. No. 2.5e-22;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGCGTCTTCTCATGACATTTGCCA 453  
DB 468 GGCTCGCTCTTGGGTCTCTTCTGGCAGCAGTGTGGATGGTGGCGCAGACTTTTGCA 527

QY 454 CCACAGACTTTCAAGAGCGGAACTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513  
DB 528 CCACAGCTCTCCAGGACGGTCTTGGGTGATCTTTTCGGCGCTCTTGGGAGGTGT 587

QY 514 TCTGCAAGTTTTTCCGTGACATGTTGGAAGCAGACACATGACATCATTCGCGCAAC 573  
DB 588 CTGCCAGGGCTTCTCGTCTCATGTGTGGAAGCAGACACACTCACACGCGCGCCC 647

QY 574 CAATGTTCAAGGGCAGCCCTGATTTGACAACTCCGCCCTTAGCCTGCTGAGGA 633  
DB 648 CAACGTCCAGCGAGATCCCGACATGACACTCACCTCTGTTGACGTGGAGTGAGCA 707

QY 634 -----TGACGTACACGGGGGTCCACCGATTTCCCGCAA 666  
DB 708 TGCTTTGAGATGTTCTCGGACGTCCCTGACGAGGAGCTGACCCGCACTGTGTCGGCTT 767

QY 667 GCTCATTCAGTTCAGCAGTACTATTTCTTGTCATCTGATCTTGTTCGGGTTCATTTG 726  
DB 768 CATGCTCTTAACAGACCTGTTTACTTTCCCATTTCTCTGTTGGCCGCTCTCTCCTG 827

QY 727 GTGTTTCAGTGCCTGTTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780  
DB 828 GTGCTTCAGTCCATCTCTTCTTGCTGCTAACGGTACGGCCACAAAGCCCTCTGGAGC 887

QY 781 CTATCGCTCTCAGTAAGAAGAGGCCATTTGGCCTCGCCCTGCACCTGGACCTTGAAGGC 840  
DB 888 CCGTGTGTCCATTCTCTTGGTCGACAGCTGTCTCTTGCCATGCACTGGACCTGGTACCT 947

QY 841 CCGTGTCCACTTATTCCTTTATGCCAGCATCCTCAGATCGCTGTGGTGTGTTTTCCTTTC 900  
DB 948 GCCCACTATGTTCTTTTCAATTAAGGACCCCGCTCAACATGATGGTGTACTTTTGTGTGC 1007

QY 901 GGAGCTGTTGGCGCTTCGGCATTTCCGATCTGTTGTTTCATGTAACCACTACCCACTGGA 960  
DB 1008 TCAGCTGTTTGGGTAACCTGTTGGCGATGTTGTTCTCGCTCAACCAAGCGGATGCC 1067

QY 961 GAAGATCGGGGCCAGCTCTGGGATGGCCATGATTTCTCGGTTGGCCAGATCCATGAGAC 1020  
DB 1068 TGTGATCCCAAGGAGGAGCGCTGACATGATTTCTTTCACCAAGCAGATCATCACGGG 1127

QY 1021 CATGACATTCGCGAGGAGTATATCAGACATTTGGTGTTCGGAGGCTTGAATTACCAGAT 1080  
DB 1128 TCGTGATGTTACCCCTGGTCTGTTCGCCAATTTGGTTTACGGGTGGATTAACCTACCAGAT 1187

QY 1081 TGAGCACCATTGTTGGCGCACCTCCTCGCCACAACCTGACAGCGGTTAGCTTACCAGGT 1140  
DB 1188 TGAGCACCATTGTTGGCTTCCCTCGATGCTCGCCACAACCTTTCAAGATCCAGCTGCTGT 1247

QY 1141 GGAACAGCTGTGCCAAGAACCAACCTGCCGTATCGGAACCC 1182  
DB 1248 CGAGACCTGTGCAAAAAGTATGTTGTCGATACCACACCAC 1289

RESULT 3  
LOCUS AR080598 1617 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 1 from patent US 5968809.  
ACCESSION AR080598  
VERSION AR080598.1 GI:10007328  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1617)  
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.-S., Thurmond,J. and Chaudhary,S.  
TITLE Methods and compositions for synthesis of long chain  
JOURNAL poly-unsaturated fatty acids  
FEATURES Patent: US 5968809-A 1 19-OCT-1999;  
Location/Qualifiers  
Source 1..1617  
BASE COUNT 310 a 470 c 410 g 427 t  
ORIGIN  
Query Match 9.5%; Score 121.6; DB 6; Length 1617;  
Best Local Similarity 49.3%; Pred. No. 2.5e-22;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGCGTCTTCTCATGACATTTGCCA 453  
DB 538 GGCTCGCTTTTGGGTCTCTTCTGGCAGCAGTGGTGGTGGCTTGGTGGCTTGGTGGCA 597

QY 454 CCACAGACTTTCAAGAACCGGNACTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513  
DB 598 TCACAGGCTTTCCAGGACCGTCTTCTGGGGTGTATCTTTCGGCGCTTCTTGGAGGTGT 657

QY 514 TCTGCAAGTTTTTTCCTGACATGTTGGAAGGACAGACACATCATTCGCGCAAC 573  
DB 658 CTGCCAGGCTTCTCTGCTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 717

QY 574 CAATGTTCAAGGGCAGCCCTGATATTGACAACTCCGCCCTTAGCCTGGTGTGAGGA 633  
DB 718 CAACGTCCAGCGGAGGATCCCGACATGACACCCACCTCTGTTGACCTGGAGTGAGCA 777

QY 634 T-----GAGGTACACAGGGCGTCCACCGATTTCCCGCAA 666  
DB 778 TGCGTTGGAGATGTTCTCGATGTTCCCGATGAGGAGCTGACCCGCACTGTGTCGGCTTT 837

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DB 838 CATGGTCCCTGAACACAGACCTGGTTTACTTCCCATTTCTCTGTTGCCGCTCTCTCCTG 897

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Db 778 TCGGTGGAGATGTTCTCGGATGCCAGATGAGGAGTGCACCGCATGTGTCGCGTTT 837
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Db 838 CATGTCCTGACACAGACCTGTTTACTTCCCATCTCTCGTTGCGCGTCTCTCTG 897
Qy 727 GTGTTTCAGTCGCTGTTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780
Db 898 GTGCTCCAGTCAGTCAATCTCTTGTGCTGCCTAACGGTCAAGGCGCCACAAAGCCCTCGGGCG 957
Qy 781 CTATCGCTCTCAGTATAAGAGAGCGCATTCGCTCGCCCTCGCTGCACTGACCTTGAAGGC 840
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## RESULT 6

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AF110510
LOCUS Mortierella alpina delta-6 fatty acid desaturase mRNA, complete cds.
DEFINITION

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ACCESSION AF110510
VERSION AF110510.1
KEYWORDS GI:6448795
SOURCE Mortierella alpina.

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ORGANISM Mortierella alpina.

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REFERENCE 1 (bases 1 to 1617)

```

```

AUTHORS Huang, Y.S., Chaudhary, S., Thurmond, J.M., Bobik, E.G. Jr., Yuan, L.,

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TITLE Chan, G.M., Kirchner, S.J., Mukerji, P. and Knutzen, D.S.
Cloning of delta12- and delta6-desaturases from Mortierella alpina
and recombinant production of gamma-linolenic acid in Saccharomyces
cerevisiae

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JOURNAL Lipids 34 (7), 649-659 (1999)
MEDLINE 99406036
PUBMED 10478922

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REFERENCE 2 (bases 1 to 1617)

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AUTHORS Knutzen, D.S.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1998) Calgene LLC, 1920 Fifth St., Davis, CA
95616, USA

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BASE COUNT 310 a 470 c 410 g 427 t
ORIGIN
Query Match 9.5%; Score 121.6; DB 8; Length 1617;
Best Local Similarity 49.3%; Pred. No. 2.5e-22;
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;
Qy 394 GGCAGTGTGTGCTGGGATGCACTATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453
Db 538 GGCCTGGCTTTGGGTCTGTTCTGGCAGCAGTCCGATGGTGGCTCAGCAGCTTTTGCA 597
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Db 718 CAACGTCCACGCGGAGGATCCCGACATGACACCCACCTCTCTGTTGACCTGGAGTAGCA 777
Qy 634 T-----GACGTACACGCGGCTCACCAGGCTCACCAGATTTCCCGCAA 666
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Qy 667 GGTCAATTCAGTTCCAGCAGTACTATTTCTTGTGTCATCTGTATCTTGTTCGGGTTCATTTG 726
Db 838 CATGTCCTGACACAGACCTGTTTACTTCCCATCTCTCTGTTTTCGCGCTCTCTCCTG 897
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Qy 781 CTATCGCTCTCAGTATAAGAGAGGCGCATTCGCTCGCCCTCGCTGCACTGACCTTGAAGGC 840
Db 958 GCGTGTGCCATCTCGTTGGTCGACAGCTGTCGTTGGATGCACTGACCTGGTACCT 1017
Qy 841 CCGTTCACATTTATTTATGCCAGCATCTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 1018 CGCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGCTGCTGCTGCTGCTGCT 1077
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Qy 1021 CATGAACATTCGGCGAGGATTTATCAGAGTTGTTTTTCGGAGCTTGAATACAGAT 1080
Db 1198 TCGTATGTCACCGCGGTCTATTTGCCAATGTTTCACGGGTGATGTAATATCAGAT 1257
Qy 1081 TGAGCACCATTGTTGGCGACCTCCCTCGCCACAACTGACAGCGGTAGTACAGGT 1140
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Qy	1141	GGACAGCTGTGCAGAGCAGACACACCTCGCGTATCGGAAACC	1182
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RESULT 7			
AF307940	1374 bp mRNA linear PLN 02-JAN-2001		
LOCUS	Mortierella alpina clone pTMACL-3 delta 6-fatty acid desaturase		
DEFINITION	Mortierella alpina clone pTMACL-3 delta 6-fatty acid desaturase		
ACCESSION	AF307940		
VERSION	complete cds.		
KEYWORDS	Mortierella alpina		
SOURCE	AF307940.1 GI:12007241		
ORGANISM	Mortierella alpina		
REFERENCE	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;		
AUTHORS	Mortierella alpina		
TITLE	1 (bases 1 to 1374)		
JOURNAL	Xing, L., Li, M., Liu, L., Hu, G. and Zhang, L.		
FEATURES	Expression of Mortierella alpina delta 6-fatty acid desaturase gene in Saccharomyces cerevisiae		
source	Unpublished		
product	2 (bases 1 to 1374)		
protein	Xing, L., Li, M., Liu, L., Hu, G. and Zhang, L.		
translation	Submitted (26-SEP-2000) Department of Microbiology, Nankai University, 94 Weijin Road, Tianjin 300071, P.R. China		
location	Location/Qualifiers		
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translation	VSAQVGNLILAVFSLNHNMPVSKIEAEVDMDFTKOIIITGRDVPGLFANFTGL		
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translation	SKMGKAQ"		
BASE COUNT	266 a	395 c	361 g 352 t
ORIGIN			
Query Match	9.3%; Score 118.4; DB 8; Length 1374;		
Best Local Similarity	49.0%; Pred. No. 1.9e-21;		
Matches 403; Conservative	0; Mismatches 386; Indels 33; Gaps 2;		
Qy	394	GGCAGTGTTCCTGGGATGCATATCAACAGATGGCTTCTCATGACATTTGCCA	453
Db	468	GGCTGCCTCTGGGTCTCTTCGCGAGCAGAGAGGATGTTGCGCAGCAGCTTTTGA	527
Qy	454	CCACGACATTTCAAGAACCGGAACCTCGTGGGACTGTTATTTGCCAATGG	513
Db	528	CCACGAGGTCTTCAGGACCGTTCTGGGGAGATCTTTTCGGCGCCTTCTTGGGAGGA	587
Qy	514	TCGCAAGGTTTTCCTGCATCTGTTGGAAGGACAGACAACTACATCATTCGCGAAC	573
Db	588	CTGCCAGGGTCTTCGTCCTCATCTGGTGAAGGACAGCAACTACCAACCGCGCC	647
Qy	574	CAATGTTCAAGGGCAGCAGCTGATATTGACAACTCCCGCTTAGCTGGTCTGAGGA	633
Db	648	CAAGTCCAGGGCAGGATCCGACATTCACACTCACCTCTGTTGACGTGGATGAGCA	707
Qy	634	-----TGACGTACACGGCGCTACCGATTTCCCGCAA	666
Db	708	TGCTTTGAGATGTTCTCGGACGCTCCCTGACGAGGAGCTGACCCGCGCTT	767
Qy	667	GCTCATTCAGTTCAGCAGTACTATTCTTGGTCTGTATCTTGTTCGGTTCATTTG	726
Db	768	CATGGTCTTAAACAGACCTGGTCTACTTCCCATCTCTCTCGTTCGCCGTCTCTC	827
Qy	727	GTGTTCCAGTGGCTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCA	780
Db	828	GTGCTCCAGTCCATCTCTTGTCTGCTTAAAGGTCAGGTCAGGCCACAAAGCCCT	887
Qy	781	CTATCGCTCTCAGTATAAGAGGAGCCATTTGGCTCGCCCTGCTGCTGCTGCTG	840
Db	888	CCGTGTCCTCATTTCCCTGTCGAGCAGCTCTCTTGGCATGCTGCTGCTGCTG	947
Qy	841	CCTGTTCCACTTATTTTATGTCGACGATCCTCAGATCGCTGTTGTTGTTGTTTC	900
Db	948	CGCCACCATGTTCTTGTTCATTAAGGACCCGCTCAACATGATGTTGTTGTTGTC	1007
Qy	901	GGAGCTGTTGGGGCTTTCGGCATTTGGGCTGGTGTTCATGAACCACTACCCACG	960
Db	1008	TCAGGCTGTTTGGGTAACCTGTTGGGATTTGCTCTCGCTCAACCAACGATGATG	1067
Qy	961	GAAGATCGGGACCCAGCTCTGGGATGGCATGATTTCTCGTTGGCCAGATCCATG	1020
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Qy	1021	CATGAACATTCGGCGAGGATTTATCAGATGTTGTTTTCGGAGGCTTTGAATACC	1080
Db	1128	TCGTGATGTTTCACTGCTGTTGTCGCACTGTTTTCAGGCTGGATTTGAATACC	1187
Qy	1081	TGAGCACATTTTGGCGGACCCCTCCCTCGCCACCACTGACAGGGTTAGTACCAG	1140
Db	1188	TGAGCACACTTGTTCCTTCGATCGCTCGCCACCACTTTTCAAGATCCAGCTGT	1247
Qy	1141	GGACAGCTGTGCCAGAGCACAACCTGCGCTATCGGAACCC	1182
Db	1248	CGAGACCTTGTGCAAAAAGTATGTTGTCGATACCAACAC	1289
RESULT 8			
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LOCUS	Mortierella alpina delta 6 fatty acid desaturase (GLD6D) gene,		
DEFINITION	complete cds.		
ACCESSION	AF465281		
VERSION	2 (bases 1 to 1374)		
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SOURCE	AF465281.1 GI:18483174		
ORGANISM	Mortierella alpina		
REFERENCE	Mortierella alpina		
AUTHORS	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;		
TITLE	Mortierellaceae; Mortierella		
JOURNAL	Liu, L., Li, M., Hu, G. and Xing, L.		
REFERENCE	1 (bases 1 to 1374)		
AUTHORS	Cloning and sequence analysis of the delta 6 fatty acid desaturase		
TITLE	gene from Mortierella alpina ATCC16266 genomic and cDNA		
JOURNAL	Unpublished		
FEATURES	2 (bases 1 to 1374)		
source	Xing, L., Liu, L., Li, M. and Hu, G.		
product	Direct Submission		
location	Submitted (04-JAN-2002) Microbiology, Naikai University, Weijiang		
organism	road 94th, Tianjin 300071, China		
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BASE COUNT	264 a	395 c	361 g	354 t		
ORIGIN						
Query Match	9.3%; Score 118.4; DB 8; Length 1374;					
Best Local Similarity	49.0%; Pred. No. 1.9e-21;					
Matches	403; Conservative 0; Mismatches 386; Indels 33; Gaps 2;					
QY	394	GGCAGTGTTCCTGGGATGCACATCAACAGATGGCTGCTTCTCATGACATTTGCCA	453			
DB	468	GGCTCGGCTCTTGGGTCTCTTCTGGCAGCAGATGGATGGTTGGCGCAGCACTTTTGCA	527			
QY	454	CCACAGACTTTCAAGAACCGGAACCTCGTGGGACTGGTATTGGCAATGG	513			
DB	528	CCACAGGCTTTCCAGGACCGTCTCTGGGGTGTATCTTTCGGCGCTCTTGGGAGGAGA	587			
QY	514	TCTGCAAGTTTTTCCGTGACATGTTGAAGGACACACATGACATCATTCGCGAAC	573			
DB	588	CTGCCAGGCTTCTCGTCTCATGTTGGAGGACACACATGACATCATTCGCGAAC	647			
QY	574	CAATGTTCAAGGGCAGCCCTGATTTGACAACTCCGCCCTTAGCCCTGTCTGAGGA	633			
DB	648	CAACGTCCACGGCGAGGATCCCGACACTGACACTCACCTCTGTGACGTGGAGTGAGCA	707			
QY	634	-----TGACGTACACGGCGCTCAGCGATTTCCCGCAA	666			
DB	708	TGCTTTGAGATGTTCTCGGAGTCCCTGACGAGGAGTGCACCCGATGTGTCGGCTT	767			
QY	667	GCTCATTCAGTTCAGCAGTACTATTTCTTGCTCATCTGTATCTTTGTCGGTTCATTG	726			
DB	768	CATGCTCTTAACAGACCTGTTCTACTTTCCCATCTCTCGTTGCGCGCTCTCTCCTG	827			
QY	727	GTGTTTCAGTGCCTGTTGACCGTGC-----GCAGTTTGAAGGACAGACATTAACAAT	780			
DB	828	GTGCTCCAGTCCATCTCTTGTCTGCTTAAACGGTCAAGCGTCAAGCCCAAGCCCTCTGGAGC	887			
QY	781	CTATCGCTCTCAGTATAAGAGGAGCCATTGGCTCGCCCTGCACTGGACCTTGAAGGC	840			
DB	888	CCGTGCGCCATTTCTTGGTGCAGACAGCTGTCTTGGCCATGCACTGGACCTGTACCT	947			
QY	841	CCTGTTCCACTTATTTTATGCCAGCATCCTACATCGCTGTTGGTGTCTTTCGTTTC	900			
DB	948	CGCCACCATGTTCTTGTTCATTAAAGACCCCGTCAACATGATGGTGTACTTTTGGTGTC	1007			
QY	901	GGAGCTGTTGGCGCTTCGGCATTCGATCGTGTGTTCATGAAACCACTACCACTGA	960			
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DB	1128	TCGTGATGTTCACTGCTGTTTCGCCAATGTTTCACGGGTGATGTAATACAGAT	1187			
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DB	1188	TGAGACCACTGTTGTCCTTCGATGCTTCGCCACAACTTTTCAAGATCCAGCCCTGCTGT	1247			
QY	1141	GGAACAGTGTGCGCAGAGCACAACCTGCCGTATTCGGAACCC	1182			

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Qy	961	GAAGATCGGGACCCAGTCTGGGATGGCCATGGATTTCTCGGTTGGCCAGATCCATGAGAC	1020	CLQSIILFVLPNGAHKSGARVPLISLVEQLSLAMHTWYLATMFLFKIDPNVMVYFL
Db	1068	TGTGATCTCCAAGGAGGAGCCGTCGACATGGATTTCTTCAACCAAGCAGATCATCACGGG	1127	VSAVCNLLAIIVFSLNHNMPVISEEAVDMDFTKQIITGRDVHPLGFANWFTGGL
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Qy	1081	TGAGCACCATTTGTCGGCGACCTCCCTCGCCACCACTGACACCGCTTAGCTACCAAGT	1140	
Db	1188	TGAGCACCATTTGTCGGCGACCTCCCTCGCCACCACTTTCAAAGATCCAGCGTGTCTGT	1247	
Qy	1141	GGACACCTGTGCGAGAGACACACCTCGCGGTATCGGAACCC	1182	
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LOCUS				
DEFINITION				1947 bp DNA linear PLN 04-FEB-2002
ACCESSION				Mortierella alpina delta 6 fatty acid desaturase (GLD6D-1) gene,
VERSION				complete cds.
KEYWORDS				
SOURCE				
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REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
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source				
gene				
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DEFINITION Mortierella alpina mRNA for delta-6 fatty acid desaturase, complete cds.
ACCESSION AB020032
VERSION AB020032.1 GI:6070339
KEYWORDS delta-6 fatty acid desaturase.
SOURCE Mortierella alpina (strain:1S-4) cDNA to mRNA.
ORGANISM Mortierella alpina
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Mortierellaceae; Mortierella.
1 (sites)
REFERENCE Sakuradani, E., Kobayashi, M. and Shimizu, S.
AUTHORS Delta6-fatty acid desaturase from an arachidonic acid-producing
TITLE Mortierella fungus. Gene cloning and its heterologous expression in
a fungus, Aspergillus
JOURNAL Gene 238 (2), 445-453 (1999)
MEDLINE 20035749
REFERENCE 2 (bases 1 to 1590)
AUTHORS Kobayashi, M., Sakuradani, E. and Shimizu, S.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Michihiro Kobayashi, Graduate School of
Agriculture, Kyoto University, Division of Applied Life Sciences;
Kitashirakawa, Oiwake-cho, Sakyo-ku, Kyoto, 606-8502, Japan
(Tel:81-75-753-6114)
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DEFINITION Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
ACCESSION AF031477
VERSION AF031477.1 GI:3088519
KEYWORDS Caenorhabditis elegans.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 1463)
AUTHORS Sayanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G., Christle, W.W., Shewry, P.R. and Napier, J.A.
TITLE Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco
JOURNAL proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
MEDLINE 97268723
PUBMED 9108131
REFERENCE 2 (bases 1 to 1463)
AUTHORS Napier, J.A., Hey, S.J., Lacey, D.J. and Shewry, P.R.
TITLE Identification of a Caenorhabditis elegans Delta6-fatty-acid-desaturase by heterologous expression in Saccharomyces cerevisiae
JOURNAL Biochem. J. 330 (pt 2), 611-614 (1998)
MEDLINE 98149727

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PUBMED 9480865  
REFERENCE 3 (bases 1 to 1463)  
AUTHORS Napier, J. A.  
TITLE Direct Submission  
JOURNAL Submitted (27-OCT-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK  
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Query Match 8.8%; Score 112.8; DB 3; Length 1463;  
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VERSION AX003603.1 GI:9927413  
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SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans  
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 1463)  
AUTHORS Napier, J. A.  
TITLE Desaturase genes and their use  
JOURNAL Patent: WO 9927111-A 1 03-JUN-1999;  
UNIV BRISTOL (GB); NAPIER JOHNATHAN A (GB)  
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ACCESSION AF078796
VERSION AF078796.1 GI:4003522
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ORGANISM Caenorhabditis elegans
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Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lewis, M., Griffiths, G., Lazarus, C.M.
and Stobart, A.K.
REFERENCE Functional identification of a fatty acid delta5 desaturase gene
from Caenorhabditis elegans
JOURNAL FEBS Lett. 439 (3), 215-218 (1998)
MEDLINE 99059458
PUBMED 9845325
2 (bases 1 to 1344)
Michaelson, L.V., Napier, J.A., Lazarus, C.M., Griffiths, G. and
Stobart, A.K.
REFERENCE Direct Submission
AUTHORS
TITLE Submitted (16-JUL-1998) Biological Sciences, University of Bristol,
Woodland Road, Bristol BS8 1UG, UK
JOURNAL Location/Qualifiers
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DEFINITION						
ACCESSION	AX020906					
VERSION	AX020906.1	GI:10044591				
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AUTHORS	1 (bases 1 to 1344)					
TITLE	Michaelson,L., Stobart,K. and Napier,J.A.					
JOURNAL	Patent: WO 933958-A 2 08-JUL-1999;					
	MICHAELSON LOUISE (GB); STOBART KEITH (GB); UNIV BRISTOL (GB);					
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 19:20:22 ; Search time 31.3774 Seconds  
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Searched: 440863 seqs, 114992915 residues  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
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US-10-191-513A-11

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; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (458)....(458)  
; OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-10-191-513A-41

Query Match 25.8%; Score 629; DB 9; Length 458;  
Best Local Similarity 33.0%; Pred. No. 5.9e-51;  
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;  
QY 4 REQHEFFPKIDGKCQIDDVLRSHPGSAITYKNMDATVTFHTHTGSKAYQWLT 63  
Db 25 KKAEEAPFLMIIDNKVDYAEFV-PDHPGGSVILTHVGKDGTDVDTFFH---PEA-AWET 79  
QY 64 ELKKECTQPEIPIDIKDDIKGIDDDVNMGTFNISEKRSQINKSFDTLRMRVAEGLMD 123  
Db 80 LANFYVGDIDESDRDKNDP-----AAEVRK-----LRTLFOSLGYD 118  
QY 124 GSPFYIRKI-----LETIFILFAFYLOVHTY-YLPSAILMGVAAQOLGWLHIEFAHQ 177

Db 119 SSKAYAFKVSFNLICINGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLADFLHHQ 178  
QY 178 LFKNRYNDLASFYVGNFLQGFSSGGWKEQHNHHAATNVVGRDGLDLVPFYATVAEHL 237  
Db 179 VFQDRFWGDLFGAFLGGVCGQGFSSSWKDKHNTTHAAPNVHGEDPDIDTHPL-LTWSEHA 237  
QY 238 NNYSDQ-----SWMTLFRQHVHTF--MLPFLRLSWLLOSIIFV-----SQ 278  
Db 238 LEMFSDVPDEELTRMWSRFVNLQNTWFFPILSFARLSWCLQSLILFVLPNGQAHKPSGAR 297  
QY 279 MPTHYDYRNTAIYEQVGLSLHAWSLGOLY-FLPDWSTRIMFELVSHLVGGFLSHVY 337  
Db 298 VP-----ISLVEQLSLAHHTWYLATMFLFKDPVNMVLVYFLVSOAVCGNLLAIF 348  
QY 338 TFNHYSEKFALESNSINYSACLOIMTTRNNRPGRFIDWLWGGLNYQIEHHLFPTMPRH 397  
Db 349 SLNNGMPVISKEEAVDMDFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPTMPRH 408  
QY 398 LNTVMPLVKEFAAANGLPYVDDYFTGFWEIEQFRNIANVAALTK 444  
Db 409 FSKIQPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

## RESULT 3

US-10-191-513A-17  
; Sequence 17, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Paridip  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Das  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295 US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (323)....(323)  
; OTHER INFORMATION: Xaa = Unknown or other at position 323  
US-10-191-513A-17

Query Match 22.2%; Score 541; DB 9; Length 323;  
Best Local Similarity 36.5%; Pred. No. 7.3e-43;  
Matches 113; Conservative 55; Mismatches 112; Indels 30; Gaps 6;  
QY 155 SAILMGVAAQOLGWLHIEFAHQHLPKNRYNDLASFYVGNFLQGFSSGGWKEQHNHHA 214  
Db 21 SAALLGLFWQCGWLADFLHHQVFDQDRFGDGLFGAFLGGVCGQGFSSSWKDKHNTTHA 80  
QY 215 TNYVGRDGLDLVPFYATVAEHLNYSQD-----SWMTLFRQHVHTF--MLPFLRL 266  
Db 81 PNHGEDPDIDTHPL-LTWSEHALEMFSDVPDEELTRMWSRFVNLQNTWFFPILSFARL 139  
QY 267 SWLQSIIFV-----SOMPTHYDYRNTAIYEQVGLSLHAWSLGOLY-FLPD 314  
Db 140 SWCLQSIIFLVPNGQAHKPSGARVP-----ISLVEQLSLAHHTWYLATMFLFKD 190  
QY 315 WSTRIMFELVSHLVGGFLSHVHTVFNHYSEKFALESNSINYSACLOIMTTRNNRPGFI 374

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Db      191  PVMNLVTLVSQAVCGNLLAIVFSLNHHNGMPVISKEEAVDMDFFTKQIITGRDVHGLFA 250
Qy      375  DLWGLGGLNYQIEHHLFPTMPRHNLNTVMPLVKEFAAANGCLPYMVDYDTFGFWLEIEQFQFN 434
Db      251  N|FTGGLNYQIEHHLFPSMRPHNFSKIQPAVETLCKYNRYHTTGMIEGTAEVFSRLNE 310
Qy      435  IANVAAKLTK 444
Db      311  VSKAASKMGK 320

RESULT 4
US-09-967-477B-8
; Sequence 8, Application US/09967477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haiping Hong
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: BNZ-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
US-09-967-477B-8

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US-10-191-513A-9
; Sequence 9, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (432)...(432)
; OTHER INFORMATION: Xaa = Unknown or other at position 432
US-10-191-513A-9

Query Match      16.8%; Score 408.5; DB 9; Length 432;
Best Local Similarity 27.7%; Pred. No. 3.4e-30;
Matches 119; Conservative 64; Mismatches 167; Indels 79; Gaps 13;

Qy 18 KWCQIDDAV-----LRSHPGGS-ATTYKNMDATVFFHTFHGSKRAYQWLT-----EL 65
Db 22 RWEIVDRKYNVISEFTRRHPGGSRVISHYAGQDATDPFAVAFHINKGLVKKYMNSLLIGEL 81
Qy 66 KKECPQEPIDIKDDPIKGIDDVNMGTENISEKSAQINKSFTDLRMVRVRAEGLMDGS 125
Db 82 SPQPSFEP-----TKNKELTDFERELRAIVERNGLMKAN 116
Qy 126 PLFYIRKILTIITILFAFYLO---YHTYLP---SAILMGVAMQQLGWLIEHFAHHOLF 179
Db 117 HVFEFLVLLH-ILLDGAAMLTWVFGTSLPFLLCVALLSVAQQAQAGWLQHDYGHLSVY 175
Qy 180 KRIYNDLASFYVGNFTLOGSSGKWEQHNHVHAATNVGVRDGDLDLVPFYATVAEHLNN 239
Db 176 .RKPKWNHLVHKFVIGHLKGASANNWNRHFQHHAKPNIFHKDPVNMLHVFVLGEWQPIE 235
Qy 240 YSDSWMVTWFRQHVHWTEMLPFLRLSLLQSLIFVYSOMPTHYDYRNTAIVEQVGLS 299
Db 236 YGKKLKLYPNHQHEVFFLIGPPLLPYFQIIM-----TMIVHKWVD 282
Qy 300 LHWAWSLGOLYFLPFDWSTRIFFLVSHLVGG-----FLLSH---VVTFNHYSEKF 347
Db 283 LAWAVS---YYIRFFITYIPFY--GILCALLFLNFIRESLHWFVYVQMNHVME-- 333
Qy 348 ALSNINMSVACIQIMTTRNMGRGFTDWLWGLNGLYOIEHHLLPTTPRPHNLNTVMPVLKE 407
Db 334 -IDQEAARDWFSSQLTACNVEGSSFFNDWFSGLHNFQIEHLLFPTTPRPHNLHKTAPLVKS 392
Qy 408 FAAANGLPY 416
Db 393 LCAKHGIEY 401

RESULT 6
US-10-191-513A-38
; Sequence 38, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:

```

APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295, US D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 465  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (432)...(432)  
OTHER INFORMATION: Xaa = Unknown or other at position 432  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (458)...(458)  
OTHER INFORMATION: Xaa = Unknown or other at position 458  
US-10-191-513A-38

Query Match 16.8%; Score 408.5; DB 9; Length 465;  
Best Local Similarity 27.7%; Pred. No. 3.8e-30;  
Matches 119; Conservative 64; Mismatches 167; Indels 79; Gaps 13;  
QY 18 KWCQIDDAV-----LRSHPGGS-AITTYKNMDATTVFHTFGSKSEAYQWLT-----EL 65  
DB 22 RMLVIDRKVNISEFTRRHPGGSRVISHYAGQATDPFVAFHINKGLVKYKMSLLIGEL 81  
QY 66 KKECTQPEIPDKDDPIKIGIDDDVNMGTNISEKSAQINKSFDTLRMRVRAEGLMDGS 125  
DB 82 SPEQSPFEP-----TKNKELTDEFRELRATVERMGLMKAN 116  
QY 126 PLFYIRKILETIFTLFAFYLO---YHTYVLP---SAILMGVAWQGLGLIHEFAHQHOLF 179  
DB 117 HVFFLLYLH-ILLDGAALWLTUWVFGTSELPFLLCALLLSAYOAGWLOHDYGHLSVY 175  
QY 180 KRYINDLASFYGNFLQGFSSGGWKEQHNVHHAATNVVGRDGLDLVFPYATVAEHLNN 239  
DB 176 RKPKNHVLHKFVIGHLKGSANWNNRHFQHHAKPNIFHKDPDVMNMLHYFVLGEWQPIE 235  
QY 240 YSODSNWMLFRQVHWHWTMLPDLRLSWLLQSLIIFVSOMPTHYDYRYNTATYEQVGLS 299  
DB 236 YGKKLKLPLYNHQHEHYFFLIGPPLIPMYFOYQIIM-----TMIVHKNWVD 282  
QY 300 LHWASLGQLYFLPDWSTRMFLVSLHVG-----FLLSH---VYTFNHYSEKF 347  
DB 283 LAWAVS-----YIRFFITYIPFY---GILGALLFLNFIRESHFWFWVTQMHVNE-- 333  
QY 348 ALSSNMSVACLIQIMTRMRGRFDLWGLGNTQIEHLLPPTMPRHNLNTVMPLVKE 407  
DB 334 -IDQAYRDWFSSQLATCNVEOSFDFNSGHLNFQIEHLLPPTMPRHNLHKLAPLVKS 392  
QY 408 FRAANGLPY 416  
DB 393 LCAKHGIEY 401

RESULT 7  
US-10-029-756-5  
Sequence 5, Application US/10029756  
Patent No. US20020108147A1  
GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.  
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
DELTA 6-DESATURASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/029,756  
FILING DATE: 21-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,254  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 83832YXXWU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-029-756-5  
Query Match 16.6%; Score 403.5; DB 12; Length 448;  
Best Local Similarity 27.0%; Pred. No. 1.1e-29;  
Matches 123; Conservative 69; Mismatches 199; Indels 65; Gaps 16;  
QY 12 FIKIDGKWCQIDDAVLRSHPGGS-AITTYKNMDATTVFHTFGSKSEAYQWLTTELKKECP 70  
DB 24 WISQGRAYDVSDMW-KDHFGSPPLKSLAGQVTDAPVAFHPAS---TW-----69  
QY 71 TQPEIPDKDDPIKIGIDDDVNMGTNISEKSAQINKSFDTLRMRVRAEGLMDG-----124  
DB 70 -----KNLDKFTG-YLKDYSVSEVSKDYRLVFEFSKMGLYDKKGHMF 114  
QY 125 SPLFYIRKILE-TIFTLFAFYLOHYTYLPSAILMGVAWQGLGLIHEFAHQHOLFKNRY 183  
DB 115 ATLCLFIAMLFAMSYGVLFCEGLVHLF---SGCLMGFLWQSGWIGHDAGHYWVYSDSR 171  
QY 184 YNDLASFVGNFLQGFSSGGWKEQHNVHHAATNVVGRDGLDLV-----FYATVAEH 236  
DB 172 LNKFMGIFAANCLSGISIGIMWKNHNAHHAACNLSLEYDPLQYIPFLVSSKFFGSLTSH 231  
QY 237 L--NNYSQDSWMTFLRWQHVHTF--MLPFLRLSWLLQSLIIFVSOMPTHYDYRYNTA- 291  
DB 232 FYEKRLTFDS--LSRFFVSQHWTFYFIMCARLNMVYOSLIMLLTK-----RNVSY 281  
QY 292 -IYEQVGLSLHAWMSLGQLYFLPDWSTRMFLVSHLVGGFLSHVVTFTNHYSEKFPALS 350  
DB 282 RAQELGCLVFSIWYPLLVSCLPNWGERIMEVIAASLSVTG-MQOVQFSLNHFSVY-VG 339  
QY 351 SNIMSNVACLIQIMTRMRGRFDLWGLGNTQIEHLLPPTMPRHNLNTVMPLVKEFAA 410  
DB 340 KPGKNNWFKEQTDGTLDISCPWMDWFGSGQFQIEHLLPFPKPRCNLRKISPYVIELCK 399  
QY 411 ANGLPYWDDYFTGFWLEIEQFRNIANVAKLTKKI 446



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; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (444)...(444)
; OTHER INFORMATION: Xaa - Unknown or other at position 444
US-10-191-513A-42

Query Match      16.3%; Score 396; DB 9; Length 444;
Best Local Similarity 26.4%; Pred. No. 5.3e-29;
Matches 123; Conservative 59; Mismatches 168; Indels 116; Gaps 17;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTKNMDATTVFTHFGSKSKEYQWLT-----EL 65
Db 34 RNLVIDKVVYNISEFTRRRHGGSKRVISHYAGQDATDPVAFHINKGLVKYKMNLSLIGEL 93
QY 66 KKECTQEPDIPDKDPIKIDVNGMTFNISEKRSQAQINKSTFD---LRMRVRAGLM 122
Db 94 SPEQSPFEP-----TKNKELTDFELRATVERMGLM 124
QY 123 DGSPLFVIRKILETIFILFAFYLO---YHTYVLP---SAILMGVAQQLGWLHIEFAHH 176
Db 125 KAHVFFLLYLLH-ILLDGAAMLTWVGTSETLPLFLLCAVLLSVAQAQAGWLQHDPEHL 183
QY 177 QLFKNRYNDLASFYGNFLQGGSGGKQKHNVHHAATNVVGRDGLDLVFPYATVAE- 235
Db 184 SVFSTKWNHLLHFVIGHLKGAPASWNHMHQHHAKPCNCRKDPDINMHPFFALGKI 243
QY 236 -----HLNNY-----SODSVNVLFRQHVHTFPLFLRLSLLQSIIF 275
Db 244 LSVELGKQKKKYPNHOHKYFFLIGPPALLPLYFQW---YIFYFYIQRKKW-----VD 294
QY 276 VSQMPHYDYRNTAIYEQVLSLHMAWSLGLYFLPDMSTRIMFLVSHLVGGFFLSH 335
Db 295 LAMWITFYVRF-----LTVPLLLGLKAFGL-----LFIVRFLESNWFV-W 335
QY 336 VVTFNHYSVEKFSALSNMINSYACLOIMTTRNMRPGRFIDWLMGGLNYQIEHHLFPTMPR 395
Db 336 VTQMNHIPM----IDHRNMDWSTQLLATCNVHKSAFNDWFSGLHNFQIEHHLFPTMPR 392
QY 396 HNLNTVMPLVKEFAAANGPLYMVDYDTGF-----WLE 428
Db 393 HNTHKVAPLVQSLCAKRGIEYQSKPLLSAFADIIHSLKESQGLWLD 438

RESULT 11
US-10-029-756-27
; Sequence 27, Application US/10029756
; Patent No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-029-756-27

Query Match      15.9%; Score 387; DB 12; Length 452;
Best Local Similarity 23.9%; Pred. No. 3.9e-28;
Matches 112; Conservative 81; Mismatches 191; Indels 84; Gaps 17;

QY 4 REQEHEFFFIKIDK-----WCQIDDAVLRSHPGGS-AITTKNMDATTVFTHFGTSK 56
Db 16 RHKSGDLWISIQKVYDCSRWA-----AEHPGGEVPLLSLAGQDVTDFATHPGTA 68
QY 57 -----EAYOWLTCLKKECTQEPDIPDKIDVNGMTFNISEKRSQAQINKS 108
Db 69 WRHLDPLFTGYIYLLKDF-----EVSEISKDYRLLNE--MSRSGIFEKKGHHIMT 117
QY 109 FTDLRMRVRAGLMDGSPFLVIRKILETIFILFAFYLOYHTYIYLPSSAILMGVAQQLGW 168
Db 118 FVGVAVMMAA-----IVYGLASESVGVH---MLCGALLGLLWIAAY 157
QY 169 LIHEFAHOLFKNRYNDLASFYGNFLQGGSGGKQKHNVHHAATNVVGRDGLDLVP 228
Db 158 VGHDSGHYQVPTRGYNRITOLIAGNLTGSIAMKWTNAHHLACHSLDYDPLQHIP 217
QY 229 FYATVAEHLNNYSQDSWVMTL-----FRQHVHTF--MLPFLRLSLLQSIIFV--- 276
Db 218 VFAVSTRLENSITSVFYGRVLKFDVAREFLVSQHTYYPVNFGRVNLFIQTFLLLTR 277
QY 277 SQMPHYDYRNTAIYEQVLSLHMAWSLGLYFLPDMSTRIMFLVSHLVGGFFLSHV 336
Db 278 RDVPDRALNL-----MGIAVFWTFFLVFVCLPNWPERFGLVLSFAVTA--IOHV 326
QY 337 -VTFNHYSVEKFSALSNMINSYACLOIMTTRNMRPGRFIDWLMGGLNYQIEHHLFPTMPR 395
Db 327 QFTLNHFSGDY-VGPPKGDWFEKQTKGTIDITCPPWMDWFFGGLQFQLEHHLFPLPR 385
QY 396 HNLNTVMPLVKEFAAANGPLYMVDYDTGFV--LEIQFRNIANYAAK 441
Db 386 GOLRKIAPLARDLCKKHGMPYR---SGFWDDANVRTIRLDAAVQ 429

RESULT 12
US-10-262-617-1
; Sequence 1, Application US/10262617
; Publication No. US20030077747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
```



; PRIOR FILING DATE: 2001-05-30

b 64 AKPNIFHKDPDVNMLHVFVLGEWQPIEYGGKKLKYLPYNHQHEYFFLIGPPLLIPMYFQY 123

QY 273 IIFVSQMPHYDYRTAIYEQVGLSHWAMSLGQYFLPDWSTRMFFELVSHLVGG-- 330  
 Db 124 QIIM-----TWVHKWVDLAWAVS-----YYIRFFITIPEV---GILGALL 163  
 QY 331 -----FLSH-----VVTNHYSVKFAALSSNMSNYACQIMTTRNMRPGRFIDMVG 380  
 Db 164 FLNFIREFLESHFVWVWVQNMHIYME---IDQEAYRDWFSQLTATCNVEQSFDFWFSGH 220  
 QY 381 LNYQIEHHLFPMPRNLNTVPLVKEFAAANGLPY 416  
 Db 221 LNFQIEHHLFPMPRNLNHLKIAPLVKSLCAKHGIEY 256

RESULT 15

US-10-191-513A-18  
 : Sequence 18, Application US/10191513A  
 : Publication No. US20030104596A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Abbott Laboratories  
 : APPLICANT: Mukerji, Pardip  
 : APPLICANT: Leonard, Amanda E.  
 : APPLICANT: Huang, Yung-Sheng  
 : APPLICANT: Tapas, Das  
 : TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
 : FILE REFERENCE: 6295, US, D3  
 : CURRENT APPLICATION NUMBER: US/10/191, 513A  
 : CURRENT FILING DATE: 2002-09-25  
 : PRIOR APPLICATION NUMBER: US 09/227, 613  
 : PRIOR FILING DATE: 1999-01-08  
 : PRIOR APPLICATION NUMBER: PCT/US98/07422  
 : PRIOR FILING DATE: 1998-04-10  
 : PRIOR APPLICATION NUMBER: US 08/833, 610  
 : PRIOR FILING DATE: 1997-04-11  
 : NUMBER OF SEQ ID NOS: 54  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 18  
 : LENGTH: 356  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: VARIANT  
 : LOCATION: (294)...(294)  
 : OTHER INFORMATION: Xaa = Unknown or other at position 294  
 : FEATURE:  
 : NAME/KEY: VARIANT  
 : LOCATION: (320)...(320)  
 : OTHER INFORMATION: Xaa = Unknown or other at position 320  
 US-10-191-513A-18

Query Match 12.8%; Score 311; DB 9; Length 356;  
 Best Local Similarity 28.7%; Pred. NO. 4.1e-21;  
 Matches 81; Conservative 41; Mismatches 112; Indels 48; Gaps 6;  
 QY 153 LPSAILMGVAVQOLGHLIHEFAHQHFNKRYNDLASFYVGNFLOGFSGGKWEQHNVHH 212  
 Db 12 LITAFVLATSOQAQAGHLQHDYGLSVYRKPKNHLVHKFVIGHLKASANWNNRHFQHH 71  
 QY 213 AATNVVGRDGLDLVFPYATVAEHLNYSQDSWVMTLFRMQ-----HVHW 257  
 Db 72 AKPNIFHKDPDVMNL-----HVFVLGEWQPIEYCKKKLKLPLYNHQHE 114  
 QY 258 TWML---PFLRLSWLQSIIFVSOMPTHYDYRTAIYEQVGLSHWAMSLGQYFLPD 314  
 Db 115 YFFLGIPPLIPFOYQIIMTIVHKNNWDLAWAVSYIRFTIPFYGILGALLFL-- 172  
 QY 315 WSTRIMFFLVSHLVGGFLLSHVVTNNHYSVEKFAALSSNMSNYACQIMTTRNMRPGRFI 374  
 Db 173 ---NFIREFLESH-----WFWVTQNMHIYME---IDQEAYRDWFSQLTATCNVEQSF 221  
 QY 375 DWLWGLNFIQIEHHLFPMPRNLNTVPLVKEFAAANGLPY 416  
 Db 222 DWFSGHLNFQIEHHLFPMPRNLNHLKIAPLVKSLCAKHGIEY 263

Search completed: July 2, 2003, 19:38:51  
 Job time : 34.3774 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 12:58:36 ; Search time 308.964 Seconds  
(without alignments)  
9293.314 Million cell updates/sec

Title: US-09-857-583-3

Perfect score: 1275

Sequence: 1 atttttttgaatgaagt.....gcggggaaggctctataaag 1275

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
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- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1275	100.0	1275	21	AA51233
2	121.6	9.5	1374	21	AA51233
3	121.6	9.5	1374	22	AAF25234
4	121.6	9.5	1617	19	AAV63624
5	121.6	9.5	1617	20	AAV63624
6	121.6	9.5	1617	21	AAV63624
7	112.8	8.8	1463	20	AAV63624
8	108.8	8.5	1344	20	AAV63624
9	108.8	8.5	1461	21	AA51232

10	107.4	8.4	1380	24	AA535090
11	71.6	5.6	1467	22	AAF25730
12	71.6	5.6	2040	22	AAF25729
13	69.8	5.5	1594	21	AAZ44832
14	63.4	5.0	1972	21	AAZ44832
15	61.6	4.8	1934	21	AAZ44832
16	60.8	4.8	1606	21	AAZ44832
17	57	4.5	1764	21	AAZ44832
18	56.4	4.4	2160	22	AAZ44832
19	56	4.4	1650	21	AAZ44832
20	56	4.4	1650	21	AAZ44832
21	56	4.4	1650	21	AAZ44832
22	56	4.4	1650	21	AAZ44832
23	53	4.2	1471	21	AAZ44832
24	52.6	4.1	2146	22	AAH15815
25	52.4	4.1	1465	21	AAZ44832
26	51.8	4.1	1684	19	AAV34398
27	51.8	4.1	1684	20	AAV34398
28	51.8	4.1	1685	17	AAV30395
29	51.8	4.1	1685	22	AAV30395
30	51.6	4.0	1686	22	AAH05343
31	51	4.0	1335	22	AAH19403
32	51	4.0	1474	21	AAZ44832
33	51	4.0	1575	24	ABL90108
34	51	4.0	1686	19	AAV63641
35	51	4.0	1686	20	AAV63641
36	51	4.0	1686	20	AAV82640
37	51	4.0	1686	21	AAV82641
38	51	4.0	1686	21	AAV82641
39	51	4.0	1686	21	AAV82641
40	51	4.0	1843	19	AAV63642
41	51	4.0	1843	20	AAV82641
42	51	4.0	1843	20	AAV82641
43	51	4.0	1843	21	AAV82641
44	51	4.0	1843	21	AAV82641
45	51	4.0	1843	21	AAV82641

#### ALIGNMENTS

RESULT 1  
AA51233  
ID AA51233 standard; cDNA; 1275 BP.  
XX  
AC AA51233;  
XX  
DT 26-SEP-2000 (first entry)  
XX  
DE E. gracilis' fatty acid delta-8 desaturase coding sequence.  
XX  
KW Fatty acid delta-8 desaturase; polyunsaturated; oil; seed;  
KW infant formula; dietary supplement; ss.  
XX  
OS Euglena gracilis.  
FH Key Location/Qualifiers  
CDS 14..1273  
FT /\*tag= a  
FT /transl\_except= (pos:71..75, aa:ValSerAlaTrp)  
FT /product= Fatty\_acid\_delta-8\_desaturase  
XX  
PN WO200034439-A1.  
XX  
PD 15-JUN-2000.  
XX  
PF 06-DEC-1999; 99WO-US28655.  
XX  
PR 07-DEC-1998; 98US-0111301.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Browse JA, Wallis JG, Watts JL;

Pythium irregulare  
C. purpureus delta  
C. purpureus delta  
B. napus sld1 DNA.  
Wheat sphingolipid  
Soybean sphingolipid  
Sphingolipid desat  
C. purpureus delta  
C. purpureus delta  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
A. thaliana sld1 D  
Florida bitterbush  
Human cDNA sequenc  
Arabidopsis thalia  
Borage delta-6 des  
Borage delta-6 des  
Borage delta-6 des  
DNA encoding Bora  
Human cDNA clone (H  
Human delta-6-des  
Human breast and o  
Human polynucleoti  
Contig 2511785 enc  
Human desaturase g  
Contig 2511785 enc  
Human delta-5-des  
Human contig DNA e  
Nucleotide sequenc  
Contig 2535 encodi  
Human desaturase g  
Contig 2535 encodi  
Human delta-5-des  
Human contig DNA e  
Nucleotide sequenc





```

Db 468 GCGTGGCTTTTGGGCTCTGTTGCGCAGCAGTGGTGGCTCAGCACTTTTGCA 527
QY 454 CCACGAGACTTCAAGAACCGGAACCTGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513
Db 528 TCACCAAGGCTTCCAGGACCGTTCTGCGGTGATCTTTTGGGGCCCTCTCTGGGAGGTGT 587
QY 514 TCTGCAAGGCTTTTCCGTCACATGTTGGAAGGAGCAGACACATGCACATCATTCGSCAAC 573
Db 588 CTGCCAGGCTTCTCTGCTCGTGGTGGAGGAGCAGACACATCAACACCGCCGCC 647
QY 574 CAATGTTCAAGGCGCAGCAGCTGATATTGACAACTCCGCCCTTAGCTGGTCTGAGGA 633
Db 648 CACGCTCCAGCGGAGGATCCGACATTCACACCCACCTCTCTGACCTGGAGTGAGCA 707
QY 634 T-----GACGTCACACGGGGCTCACCGATTTCCGCAAC 666
Db 708 TCGTTGGAGATGTTCTCGGATGCCAGATGAGGAGCTGACCCGATGCTGCGGTTT 767
QY 667 GCTCATTCAGTCCACGACGACTATTCTTGGTCACTGTATCTTGTGGGTTCATTG 726
Db 768 CATGGTCCGAAACCACTGGTTTACCTCCCATCTCTGCTTTGCCGCTCTCCCTG 827
QY 727 GTGTTTCCAGTGGCTGTTGACCGTGC-----GCAGTTTGAAGGACAGATAACCAATT 780
Db 828 GTGCTCCAGTCCATCTCTTGTGCTGCTTAAGGTGAGGCTGAGCCCAAGCCCTCGGGCG 887
QY 781 CTATCGCTCTCAGTATAGAAGGAGGCGCATTTGGCCCTGCGCTGCATGGACCTTGAAGGC 840
Db 888 GCGTGTGCCCATCTCGTTGCTGAGCAGCTGTGCTTGCATGCACTGGACCTGGTACCT 947
QY 841 CTTGTTCCACTTATCTTATGCCCCAGCATCCCTCATCTGCTGTTGTTTTCGTTTC 900
Db 948 CGCCACCATGTTCTCTTATCAAGGATCCCGTCAACATGCTGGTGACTTTTGGTGTCT 1007
QY 901 GGAGCTGGTGGCGGCTTGGCAATTGCGATCGTGGTTCATGAACCACTACCCACTGGA 960
Db 1008 GCAGGCGGTGGGGAACCTGTTGGGATCGTGTCTCCCTCAACCAACGATGCTGCC 1067
QY 961 GAAGATCGGGGACCCAGTCTGGGATGCCATGATGCTCGTGGTGGCCAGATCCATGAGAC 1020
Db 1068 TGTGATCTCGAAGGAGGCGGCTGATATGATGATTTTTCACGAAGCAGCATCATCGGG 1127
QY 1021 CATGAACATTCGCGAGGATATACAGATGCTGTTTTCGAGGCTTGAATACAGAT 1080
Db 1128 TCGTATGTCACCCCGGCTTATTTGCCAACTGGTTCACGGGTGATTTGAATCATCAGAT 1187
QY 1081 TGAGCACCATTTTGGCCGACCCCTCCCTCGCCACACCTGACAGCGGTTAGCTACCAAGT 1140
Db 1188 CGAGCACCATCTGTTCCCTTCGATGCTCGCCACACTTTTCAAGATCCAGCTGCTGT 1247
QY 1141 GGAAAGCTGTGCGAAGCAGACACCTCGCGTATCGGAACCC 1182
Db 1248 CGAGACCCCTGTGCAAAAGTACAATGTCCGATACCAACAC 1289
```

## RESULT 4

AAV63624  
ID AAV63624 standard; cdna; 1617 BP.

AC AAV63624;

XX 15-FEB-1999 (first entry)

DT cDNA encoding a delta-6 desaturase enzyme.

DE Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;  
XX malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;  
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;  
KW cholesterol level; endometriosis; premenstrual syndrome;  
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;  
KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

OS Mortierella alpina.  
XX  
FH Key Location/Qualifiers  
FT CDS 71..1444  
FT /\*tag= a  
FT /product= delta-6 desaturase  
XX  
PN W09846763-A1.  
XX  
XX 22-OCT-1998.  
XX 10-APR-1998; 98WO-US07126.  
XX 11-APR-1997; 97US-0834655.  
XX (ABBO ) ABBOTT LAB.  
XX (CALJ ) CALGENE LLC.  
XX Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;  
XX Thurmond J;  
XX WPI; 1998-594582/50.  
XX P-PSDB; AAW841137.  
XX New Isolated fatty acid desaturase enzymes - used for the production  
XX of polyunsaturated fatty acids for use in, e.g. pharmaceutical  
XX compositions, nutritional compositions, cosmetics or animal feed  
XX Claim 1; Fig 3A-E; 165pp; English.  
XX  
XX The present sequence encodes a Mortierella alpina fatty acid delta-6  
XX desaturase enzyme. The enzyme sequence is used in the methods of  
XX the invention. The specification describes methods for desaturating a  
XX fatty acid and for producing a desaturated fatty acid by expressing  
XX increased levels of a desaturase. The present desaturase is an enzyme  
XX which introduces a double bond carbons 6 and 7 from the carboxyl end of  
XX a fatty acid molecule. The enzyme can be used for desaturating fatty  
XX acids. The enzyme can be used to produce polyunsaturated fatty acids,  
XX which can be used for treating malnutrition, in pharmaceutical  
XX compositions, in cosmetics or in animal feed. The polyunsaturated fatty  
XX acids can be used for treating e.g. restenosis after angioplasty,  
XX inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes  
XX or eczema or reduce blood pressure. They can also be used to inhibit  
XX platelet aggregation, cause vasodilation, lower cholesterol levels,  
XX inhibit proliferation of vessel wall smooth muscle and fibrous tissue,  
XX reduce or prevent gastro-intestinal bleeding and other side effects  
XX caused by non-steroidal anti-inflammatory drugs, prevent or treat  
XX endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis  
XX and chronic fatigue after viral infections, treat AIDS, multiple  
XX sclerosis, acute respiratory syndrome, hypertension and inflammatory skin  
XX disorders.  
XX  
SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;

Query Match 9.5%; Score 121.6; DB 19; Length 1617;  
Best Local Similarity 49.38; Pred No. 9.4e-27;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;  
QY 394 GGCAGTGTGCTGGGATGCACATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453  
DB 538 GGCTGCGCTTTTGGTCTGTTCTGGCAGCAGTGGGATGTTGGCTCAGCACTTTTGCA 597  
QY 454 CCACCACTTTCAAGAACCGGAACTCGTGGACATCGTGGAGCTGGTATTTGGCAATGG 513  
DB 598 TCACCACTGCTTCCAGGACCGCTTTCTGGGGTGATCTTTTCGGGCGCTTCTTTGGGAGGTGT 657  
QY 514 TCTCAAGTGTTCCTGTCACATCTGGAAGCAGACACATGCACATCATTCGCGAAC 573  
DB 658 CTGCGAGGGTCTCTGCTCTGTTGGAGGAGCAGACACATCTACACGCGCGCCC 717  
QY 574 CAATGTTCAAGGGCAGCAGCCCTGATATATGACAACTCCCGCCCTTAGCTGTGCTGAGGA 633  
DB 718 CAACGTCACGGCAGGATCCCGACATTCACCCACCTCTGTTGACTGAGTGAGCA 777

Qy	634	T-----GACGTCACAGCGGCGCTACCGATTTCCTCCGCAA	666
Db	778	TGCGTTGGAGATGTTCTCGGATGTCACAGATGAGGAGCTGACCCCGCATGTGGTCGCGTTT	837
Qy	667	GCTCATTTACAGTTCACAGCAGTACTATTCTTGGTGCATCTGTAATCTTGTTCGGGTTCAATTTG	726
Db	838	CATGGTCTCGAACACAGACCTGGTTTACTTCCCATCTCTCGTTTTCGCCGCTCTCTCCTG	897
Qy	727	GTGTTTTCCAGCGCGTGTGACCGTGC-----GCAGTTTGAAGACACAGATTAACCAATT	780
Db	898	GTGGCTTCAGTGCATCTCTTTGTGCGCTAACGGTCAGGCCACACGCCCTCGGGCGCG	957
Qy	781	CTATCGCTCTCAGTATAAGAGGAGGCGCATTTGGCCTCGCCCTGCACATGAGACCTTGAAGGC	840
Db	958	CGGTGTGCCCATCTCGTTGGTCGAGCAGCTGTGCGTTGCGATGCGACTGGACCTGGTACCT	1017
Qy	841	CCTGTTCCACTATTCTTTATGCCCCAGCATCCACATCGCTGTGTGTTGTTTTCGTTTC	900
Db	1018	CGCCACCATGTCTCTGTTCTATCAAGGATCCCGTCACATGCTGGTGACTTTTGTGGTGC	1077
Qy	901	GGAGCTGTTGGCGGCTTCGGCATTCGGATCGTGGTGTTCATGAACCACCTACCCACTGGA	960
Db	1078	CGAGCCGGTGTGCGGAACCTTGTGGCGATCGTGTCTCGCTCAACCACCAACGGTATGCC	1137
Qy	961	GAAGATCGGGAGCCAGCTCTGGGATGCCATGGAATTCGCTTGGCCAGATCCATCAGAC	1020
Db	1138	TGTGATCTCGAAGGAGGAGCGGTGCGATATGGATTCTTCACGAAGCAGATCATCAGGG	1197
Qy	1021	CATGAACATTCGGCGCAGGATATATCAGAGATTGGTTTTTCGGAGGCTTGAAATTACAGAT	1080
Db	1198	TCGTGATGTTCCACCCGGGTCTATTTCGCAACTGGTTTCACGGGTGGATTGAACATATCAGAT	1257
Qy	1081	TGAGCACCATTTGTGGCGGACCCCTCCCTCGCCACAACTCGACAGCGGTTAGCTACCAAGT	1140
Db	1258	CGAGCACCACTGTTCCCTTCGATGCCCTGCCACAACTTTTCAAGAGATCCAGCGCTGCTGT	1317
Qy	1141	GGAAACGCTGTGCCAAGACACAACTGCCGTATTCGGAACCC	1182
Db	1318	CGAGACCCCTGTGCAAAAGTATCAATGTCCGATACCAACCCAC	1359

## RESULT 5

**AAX00889**  
ID AAX00889 standard; DNA; 1617 BP.

DT 26-MAR-1999 (flrst entry)

DE Mortierella alpina delta 6 desaturase encoding DNA.

Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;  
 polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;  
 stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;  
 dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;  
 rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;  
 diabetes; cosmetic; animal feed; ss.

OS Mortierella alpina.

xx	Key	Location/Qualifiers
FH		

FT	CDS	71..1443

FT /\*tag= a

```
FT      /product= "delta 6 desaturase"
```

PN WO9846764-A1.

22-OCT-1998.

10-APR-1998: 98WO-US07421.

XX  
PR 24-OCT-1997: 97US-0956985.



QY 727 GTGTTTCCAGTCCGTTGACCGTGC-----GCAAGTTGAAGGACAGAGATAACCAATT 780  
 DB 898 GTGCTCCAGTCCATCTCTTTGCTGCTAACGGTCAGGCCCAACGCCCTCGGGCGC 957  
 QY 781 CTATCGCTCTCAGTATAAAGAGAGCCATTGGCTCGCCCTGCACTGGACCTTTGAAGGC 840  
 DB 958 GCGTGTGCCCATCTCGTTGGTCGAGCAGCTGCTGCTGGCATGCACTGGACCTGGTACCT 1017  
 QY 841 CCGTGTCCACTTATCTTTATGCCAGCATCTCAGATCGCTGTGGTGTCTTTTCGTTTC 900  
 DB 1018 CCCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGCTGTTACTTTTGGTGTC 1077  
 QY 901 GGAGCTGTTGGCGGCTCGGATTCGCGATTCGATGCTGGTGTTCATCAACCACTACCCACTGGA 960  
 DB 1078 GCAGCGGTGTCGGGAACTTGTGGGATCGTGTCTCGCTCAACCAACGATATGCC 1137  
 QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATGATCTCGTGGCCAGATCCATGAGAC 1020  
 DB 1138 TGTGATCTCGAAGGAGGCGGTGATGATGATGATTTCTTACGAAGCAGATCATCAGGG 1197  
 QY 1021 CATGAACATCCGCGAGGATATACAGATGTTGTTTCGAGGCTTGAATACAGAT 1080  
 DB 1198 TCGTATGATCCACCGGGTCTATTTGCCAACTGGTTCACGGGTGATTTGAACATATCAGAT 1257  
 QY 1081 TGAGCACCATTGTTGGCCGACCTCCCTCGCCACACCTGACAGCGGTTAGCTACCAGCT 1140  
 DB 1258 CGAGCACCATTGTTCCCTTCGATGCTCGCCACAACTTTCAAGATCCAGCTGCTGT 1317  
 QY 1141 GGAACAGCTGTCCGAGAACACAACTGCCGTATCGGAACCC 1182  
 DB 1318 CGAGACCTGTGCAAAAGTACAATGTCGATACCAACACAC 1359

RESULT 6  
 ID AAA09430  
 AC AAA09430;  
 DT 10-AUG-2000 (first entry)  
 DE M. alpina delta-6, fatty acid desaturase coding sequence.  
 KW delta-6 desaturase; gamma-linolenic acid; biosynthesis;  
 KW transgenic insect cell; polyunsaturated long chain fatty acid;  
 KW antiinflammatory; antirheumatic; antidiabetic; antipsoriatic;  
 KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;  
 KW anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;  
 KW antiaggregant; vasotropic; ss.  
 OS Mortierella alpina.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 71..1443  
 FT /\*tag= a  
 FT /\*product= delta-6\_desaturase  
 XX  
 PN WO200020602-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 29-SEP-1999; 99WO-US22686.  
 XX  
 PR 05-OCT-1998; 98US-0103110.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Mukerji P, Huang Y, Parker-barnes JM, Das T;  
 XX WPI; 2000-328935/28.  
 DR P-PSDB; AAY92599.  
 XX  
 PT Novel transgenic insect cells comprising a nucleotide sequences which

PT encode delta-6-desaturase or delta-12- desaturase, useful for producing  
 PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid  
 XX  
 PS Example 2; Page 144-145; 170pp; English.  
 XX  
 CC The fatty acid desaturases are able to catalyze the conversion of oleic  
 CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of  
 CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells  
 CC comprising a nucleotide sequence which encodes a polypeptide comprising  
 CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6  
 CC desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are  
 CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated  
 CC from the recombinant insect cells are also claimed. Production of  
 CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many  
 CC advantages, as insect cells have greatly simplified lipid compositions,  
 CC are not subject to external variable fluctuations, and can easily be  
 CC maintained and manipulated. The oils are used in pharmaceutical  
 CC compositions, infant formulas, dietary supplements or substitutes, and  
 CC cosmetics (all claimed). The PUFA supplements have antinflammatory,  
 CC antirheumatic, antidiabetic, antipsoriatic, osteopathic, cytostatic,  
 CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,  
 CC hypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic  
 CC activity.  
 XX  
 SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;  
 Query Match 9.5%; Score 121.6; DB 21; Length 1617;  
 Best Local Similarity 49.3%; Pred. No. 9.4e-27;  
 Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;  
 QY 394 GGCAGTGTGCTTGGGATGCACATATCAACAGATGGGTGCTTCTCATGACATTTGCCA 453  
 DB 538 GCGTGGCTTTGGGTCTGTTGGCAGCAGTGGGATGGTGGCTCAGACATTTTGCA 597  
 QY 454 CCACAGACTTTTCAAGAACCGGAACCTGGAACACCTCGTGGGACTGTTATTTGCAATGG 513  
 DB 598 TCACCAAGTCTTCCAGGACGTTTCTGGGTGTATCTTTTCGGCGCTCTTTGGAGGTG 657  
 QY 514 TCTGCAAGTGTTCGTCGACATGTTGGAAGGACAGACAAATGCACATATTCGGCAAC 573  
 DB 658 CTGCCAGGCTTCTCTGCTCTGCTGGTGAAGGACAAACACACTCACCACGCGCGCC 717  
 QY 574 CAATGTTCAAGGACGACGCTGATATTGACACCTCCCGCTTACCTGGTCTGAGGA 633  
 DB 718 CACGTCACGCGGAGGATCCGACATGACACCCACCTCTGTTGACCTGGATGAGCA 777  
 QY 634 T-----GACGTACACAGGCGGTACCGATTTCCCGCAA 666  
 DB 778 TCGTGTGGAGATGTTCTCGGATGTCAGATGAGGAGCTGACCGCATGTGGTCGCTT 837  
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 DB 838 CATGTCCTGAACACAGACCTGTTTACTTCCCATTTCTCTCGTTTCCCGCTCTCTCTG 897  
 QY 727 GTGTTTCCAGTGGTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780  
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 QY 901 GGAGCTGTTGGCGGCTTCGCGATTCGCGATTCGATGCTGGTGTTCATCAACCACTACCCACTGGA 960  
 DB 1078 GCAGCGGTGTCGGGAACTTGTGGGATCGTGTCTCGCTCAACCAACGATATGCC 1137  
 QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATGATTTCTCGGTTGGCCAGATCCATGAGAC 1020  
 DB 1138 TGTGATCTCGAAGGAGGCGGTGATGATGATGATTTCTTACGAAGCAGATCATCAGGG 1197



QY 1021 CATGAACATTCGGAGGAGGATTATCACAGATTGGTTTTTCGGAGGCTTGAATACCAAGAT 1080  
 Db 1198 TCCTGATGTCACCGGGTCTATTTGGCCAACTGGTTCACGGGTGGATTGAACATATCAGAT 1257  
 QY 1081 TGAGCACCATTGTTGGCGGACCTCCCTCCGCCCAACCTGACAGCGGTTAGCTACCAAGT 1140  
 Db 1258 CGAGCACCATTGTTCCCTTCGATGCGCTCGGCCCAACTTTTCAAGATCCAGCGCTGCTGT 1317  
 QY 1141 GGAACAGCTGTCAGAGACACAACTGCGCTGCGGAACCC 1182  
 Db 1318 CGAGACCCCTGTGAAAAGTACAAATGTCGATACCCACACAC 1359

RESULT 7

AAAX76589  
 ID AAX76589 standard; cDNA; 1463 BP.

XX AC AAX76589;

XX DT 11-AUG-1999 (first entry)

XX DE Caenorhabditis elegans Delta 6 desaturase Ced6.1 encoding cDNA.

XX KW Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Ced6.1;  
 KW gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic acid;  
 KW OPA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;  
 KW hypercholesterolemia; diabetic neuropathy; viral infection; acne;  
 KW hypertension; cirrhosis; cancer; ss.

XX OS Caenorhabditis elegans.

XX FH Key Location/Qualifiers  
 XX CDS 11..1342

XX FT /\*tag= a

XX PN WO927111-AL.

XX PD 03-JUN-1999.

XX PF 24-NOV-1998; 98WO-GB03507.

XX PR 24-NOV-1997; 97GB-0024783.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Napier JA;

XX DR WPI; 1999-370905/31.

XX DR P-PSDB; AAY17751.

XX PT Desaturase enzymes, the genes encoding them and their uses

XX PS Claim 29; Fig 1; 44pp; English.

CC The present sequence encodes Caenorhabditis elegans Delta 6 desaturase,  
 CC designated Ced6.1. Desaturase enzymes (I) may be used as immunogens to  
 CC raise and select antibodies (which may be used in immunoassays, and  
 CC diagnostic tests to detect the presence of (I) in a sample, or to purify  
 CC (I)) or as a selectable marker for transformation, especially  
 CC transformations involving plants. (I) can be used to produce gamma-  
 CC linolenic acid (GLA) (and derivatives of it), which is a high value  
 CC plant fatty acid that is widely used in medicine for the preparation of  
 CC compositions for treating disorders associated with deficiencies in GLA  
 CC or deficiencies in metabolites derived in vivo from GLA, such as  
 CC octadecatetraenoic acid (OTA) and eicosanoids. Disorders that may be  
 CC treated with GLA and OTA include eczema, mastalgia, atherosclerosis,  
 CC hypercholesterolemia, coronary disease, diabetic neuropathy, viral  
 CC infections, acne, hypertension, cirrhosis and cancer. The nucleotide  
 CC sequences (II) encoding (I) may be used as probes or primers. Probes may  
 CC be used to identify and purify nucleic acids and so may be used in  
 CC diagnosis to detect the presence of (II) in a sample. Primers are useful  
 CC for amplifying DNA by polymerase chain reaction (PCR). (II) may also be

CC used to prepare an organism that is either chill resistant or that  
 CC accumulates GLA or metabolites derived from GLA. Hybridizing DNA  
 CC molecules may be used as anti-sense molecules to alter the expression of  
 CC (II) by binding to it and preventing transcription. Hybridizing  
 CC molecules may also be provided as ribozymes which regulate expression by  
 CC cleaving RNA molecules.

XX Sequence 1463 BP; 445 A; 288 C; 277 G; 453 T; 0 other;

QY Query Match 8.8%; Score 112.8; DB 20; Length 1463;  
 Db Best Local Similarity 48.3%; Pred. No. 4.8e-24;  
 QY Matches 389; Conservative 0; Mismatches 402; Indels 15; Gaps 2;

QY 382 GTATTTTCATTTGGGCGAGTGTGCTGGGATGCATATCAACAGATGGCTGGCTTCTCA 441  
 Db 454 GTATATTACTTCTGCATGTTTTATTAGCACTTGGCAAAATTCGGATGGTTAACACA 513  
 QY 442 TGACATTTGGCACCACCAGCACTTTCAAGAACCGGAACCTGGAAACACCTCGTGGGACTGT 501  
 Db 514 TGAGTTCTGCCATCAACAGCAACAAAGAACAGACACCTTGAATGATACTATTCTTGT 573  
 QY 502 ATTTGGCAATGGTCTGCAAGGTTTTTCGGTGACATGTTGGAAGGACAGACACAATGCA 561  
 Db 574 CTTTGGTAATTTCTTACAAGGATTTTCAAGAGATTTGGTGAAGGACAAAGCACTCA 633  
 QY 562 TCATTCGGCAACCAATGTTCAAGGGCAGCACCTGATATTGACAAACCTCCCCCTTACC 621  
 Db 634 TCAGCTGCCCAAAATGTAATGATCATGACGGGTGATATCGACTTGGCACCCTTTTCG 693  
 QY 622 CTGCTCTGAGGATGACGTCACACGGGGTCAACCACTT-----CCCGCAAGCT 669  
 Db 694 ATTTATTCAGGAGATTTTGCAAGTATAAGGCCAGCTTTGAAAAGCAATTCACAGAT 753  
 QY 670 CATTCAGTTCCAGCAGTACTATTTCTTGGTGCATCTGTATCTTGTTCGGTTCATTTGGTG 729  
 Db 754 TGTACCATATCAACATCTCTATTTACCGCAATGCTTCCAATGCTCCCTTCTCATGGAC 813  
 QY 730 TTTCCAGTGGGTGTTGACCGTGGCAGTTTCAAGGACAGATACCAATCTATCGCTC 789  
 Db 814 TGGTCAGTCAGTTCAATGGGTATTCAAGAGATCAAAATGGAGTACAAGGCTATCAAG 873  
 QY 790 TCAGTATAAGAAAGGAGGCCATTGGCTCGCCCTGCACCTGGACCTTGAAGGCCCTCTTCCA 849  
 Db 874 AATGCAATTCGGGAGCAACAAATTTGTTGGACATTTGGGCTT---GGGTATCTATCA 930  
 QY 850 CTTATCTTTATGCCAGCAATCCCTACATCGCTGTGTGTGTTTTCGTTTCGGAGCTGT 909  
 Db 931 ATTGTTCTTATTACCAACATGGCCACTTCGGGTTGCTTATTATTATTATTTTACAAATGG 990  
 QY 910 TGGCGGCTTCGGCATTTGGGATCGTGGTGTTCATGAACCACTACCCACTGGGAGAGATCGG 969  
 Db 991 AGGAGGCCCTTTTGATTTGCTACGTAGTACATTTCAACCACTAACTCTGTGTGAATATCC 1050  
 QY 970 GGACCCAGTCTGGGATGGCCATGGATTCTCGGTTGGCCAGATCCATGAGACCAATCAAT 1029  
 Db 1051 AGCCAAATCTCGAATTTTAAACAATTCGCCGCTCTTCAAAATTTTGACCAACACGCAAT 1110  
 QY 1030 TCGCGAGGAGGATTATCACAGATTTGTTTTCGGAGGCTTGAATTTACCAGATTGAGCACA 1089  
 Db 1111 GACTCCATCTCCATTCATTGATTGTTGGGTGGACTCAATATATCATGATCGAGCACA 1170  
 QY 1090 TTTTGGCGGACCTCCCTCGCCCAACCTGACAGCGGTTAGCTACCAAGGTTGGAACAGCT 1149  
 Db 1171 CTTTCTCCCAACAATGCCACCTTGAATCTGAATGCTTGAATATGTGAAAAGATG 1230  
 QY 1150 GTGCCAAGCAGCAACCTGCGGTATC 1175  
 Db 1231 GTGCAAGAGAAATAATCTTCTTACC 1256

RESULT 8

AAAX86961

ID AAX86961 standard; cDNA; 1344 BP.





```
Db 574 GGCAACCTTATCGCTGCCTCGTGGCAACCCCTGGCAGGCTTCACGCTGCAGTGTGG 633
Qy 542 AAGCAGACACATGACATCATTCGGCAACCAATGTTCAAG-----585
Db 634 AAGAACAAGCACAACTGCAACGCGGTCCGCAACCTGCACAGCGCAAGGAGGAGGC 693
Qy 586 -----GCACAGCCCTGATATTGACAACTCCCCCTTAGCCTGCTGAGGATGAGCTC 640
Db 694 TTCTCGCGACCCGACATCGACACCATCGCGTCTGCGTGTCTAAGGATGCG 753
Qy 641 ACACGGGC-----GTACCGATTTCCCGAAGCTCATTCAGTTCACAGCACTACTATTC 694
Db 754 CGCAAGCGTTCGAGTCGGCGCACGCGCTTCCTCATCGCAACCGAGGCTTCTATAC 813
Qy 695 TTGGTCACTGATCTATGTTGGGCTTCATTGTTGTTCCAGTCCGCTGTTGACCGTGGC 754
Db 814 TTCCCGTGTGTGTCGCGCGCTGAGTGGCTCGCGAGTCTGTTCTTCTACGTTTC 873
Qy 755 AGTTGAAGACACAGAGATAACCAATCTATCGCTCTCAGTATAGAAGGAGGCTATGGC 814
Db 874 ACCGAGTTCGTTCCGCTATTCGACAAGGTCGAGTTCGACGCGGAGAGCGCGGT 933
Qy 815 CTGCGCTGCACTGGACCTTGAAGCCCTGTTCACATTAATCTTTATGCCAGCATCCTC 874
Db 934 CTGATCTGCACTACATCTGCACTCGGCTCGGCTACCTCTGCAACATGAGCTGTT 993
Qy 875 ACATCGCTGTGTTGTTTTCGTTTCGAGCTGTTGGCGCTTCGCGCATTCGATCGTG 934
Db 994 GAGGCGTGGCATACTTCTCTATGGCGCGGCTCTGCGGCTTCTGCTGCGCGTGGT 1053
Qy 935 GTGTTATGAACCACTACCCACTGGAAGATCGGACCCAGCTCGGATGGCATGGA 994
Db 1054 TTGAGTATGGCCACAGCGCATGTCGTTGACAGCGCGGACCAAG-----CCGAC 1107
Qy 995 TTCTCGTGGCCAGATCCATGAGACCATGACCATTCGGGAGGATATCACAGATTGG 1054
Db 1108 TTCTGCGAGCTGAGGTGACACGACGCAACATCGCGGCTCGGTATTCATGAGCTGG 1167
Qy 1055 TTTTTCGAGGCTTGAATTACAGATTGAGCACCATTGTTGGCGGACCTCCCTCGGCAC 1114
Db 1168 TTCCGCGTGGTGAAGTAACTACAGATGACCATACCTGTCCGCTCGTGGCGGCAC 1227
Qy 1115 AACCTGACAGCGGTACCTACCGGTGGAACAGCTGTCAGAGAGCAACCTCCGCTAT 1174
Db 1228 AACTTGCAAGGTCAAGTCTCATCAAGTCTGATGCAAGGATTCGACATCCCGTTC 1287
Qy 1175 CGGAACCCGTGCCCCATGAAGGTTGGTCACTCTGCTGCGCTATCTGCGGTTTC 1231
Db 1288 CAGGAGACCGGCTTCTGGGAGGCGATCTACGAGTCTGGACCACTGGCGGACATC 1344
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## RESULT 11

AAF25730  
ID AAF25730 standard; DNA; 1467 BP.

XX AC AAF25730;

XX DT 06-APR-2001 (first entry)

XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.

XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;  
transgenic plant; plant oil; triglyceride; nutrition; animal feed;  
cosmetic; ds.

XX OS Ceratodon purpureus.

XX FH Location/Qualifiers  
10..1461

XX FT /\*tag= a

XX FT /product= "delta6-acetylenase/delta6-desaturase"

PN WO200075341-A1.  
XX PD 14-DEC-2000.  
XX PF 07-JUN-2000; 2000WO-EP05274.  
XX PR 07-JUN-1999; 99DE-1025718.  
XX PR 22-DEC-1999; 99DE-1062409.  
XX PA (BADI ) BASF AG.  
XX Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;  
WPI: 2001-112150/12.  
XX P-PSDB: AAB46436.  
XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for  
producing plant oils with increased content of unsaturated fatty acids  
Claim 1a; Page 46-48; 69pp; German.  
XX This invention describes a novel isolated nucleic acid (I) encoding  
polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase  
activity. The invention also describes (a) amino acid sequences encoded  
by (I); (b) an expression cassette (EC) containing (I) linked to one or  
more regulatory sequences; (c) a vector containing (I) and EC; (d)  
organisms containing (I), EC or the vectors of (c); (e) preparation of  
unsaturated fatty acids (A) or triglycerides (TG) with increased content  
of (A) by introducing (I) or EC into an oil-producing organism; (f)  
production of (A) or TG by using (Ia); and (h) (A) and TG produced by  
method (g). (I) are used to produce transgenic plants (or other  
organisms) that produce oils or triglycerides (TG) with increased content  
of unsaturated fatty acids (A) and to isolate related sequences by  
homology screening. (A), or TG containing them, are useful in human  
nutrition (e.g. infant foods), animal feeds, pharmaceuticals and  
cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,  
can be used to suppress expression of (II), resulting in oils with  
increased content of saturated fatty acids.  
XX SQ Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 other;

Query Match 5.6%; Score 71.6; DB 22; Length 1467;  
Best Local Similarity 45.4%; Pred. No. 2.9e-11;  
Matches 352; Conservative 0; Mismatches 409; Indels 15; Gaps 2;  
Qy 401 TTGCTGGGATGCACTATCAACAGATGGCTGGCTTTCTCATGACATTTGCCACACCAG 460  
Db 604 TTGATGGTCTCTTCGTCACACAGTGTGGATGGCTTGCCCATGATTCTTCTCATCAACAG 663  
Qy 461 ACTTTCAGAACCCGAACTGGAACACCTCGTGAGCTGGTATTTGGCAATGGTTCGAA 520  
Db 664 GTCTTTGAGAACCCGTACCGCAACTCTCTTTGGCTATTTGTCGGCAATGGCTGTT 723  
Qy 521 GGTTTTCCGTCACATGTTGGAAGACAGACACATGCAATCTCGGCAACCAATGTT 580  
Db 724 GGCTTTAGTATCATGTGGAGACGACACACATTCATCATCTGCTCCGATGAG 783  
Qy 581 CAAGGACGACCCCTGATATTGACAACCTCCCGCTTTAGCTGCTGTAGAGATCACCTC 640  
Db 784 TGCAGCACACAGTACACACCTCTAGACGAAGACATTTGATCTCTCCCATCATTTCCCTGG 843  
Qy 641 ACACGGGCTGACCGATTTCCCGCAAGCTATTTCAGTTCAGGACGAGTACTATTTCTTGGTC 700  
Db 844 AGCAAGGAAATTTTGGCCACCGTTGAGAGCAAGAGAAATTTCCGAGTCTCTCAATATCAG 903  
Qy 701 ATCTGTATCTGTTGCGGTTCATTTGGTGTTCAGTGGTTCACCGTGGTTCAGCTGCTG 760  
Db 904 CACTACATGATTTCTGCTCTATTGTTATGCGCCGGTACAGTTGACATTTTGGAAAGTTG 963  
Qy 761 AAGGACAGAGATAACCAATTTCTATCGCT---CTCAGTATAAGAGGAGGCCATTTGGCCTC 817

Db 964 CTCCTTCATCTCACTGATTTGAGCAGCAGCAGGATGTATAGAGAGGGAACAGTT 1023  
QY 818 GCCCTGCACCTGGACCTTGAAGGCCCTGTTCCACTTATTCCTTTATGCCAGCATCCTCACA 877  
Db 1024 GCTTTTTCACCTACGCGCTGCTTTCAGTTCGGCTGCGTTCATATTTTGGCGGGTGCCTAAG 1083  
QY 878 TCGCTGTTGTTGTTTTCGTTTCGGAGCTGTTGGCGGCTTCGCGCATTCGATCGTGGTG 937  
Db 1084 CTTCTTCGGTGGATGGTAGCAACTGAGCTTGTGGCGGTTGTTTGGGATTCGTTGTT 1143  
QY 938 TTCTATGAACCACTACCCACTGGGAAGATCGGGAGCCAGCTCTGGATGGCCATGGATTC 997  
Db 1144 ACCTTGATCACAATGAAGAGGTTTACATGAATCG-----AAGACTTC 1191  
QY 998 TCGGTTGGCAGATCCATGAGACCATGAACATTCGGCGAGGGATTTATCAGATTTGTTT 1057  
Db 1192 GTGAGAGCCAGGTTATTACCAACCCGTAACACCAAGCGAGGCTGTTTCAAGATTGGTTC 1251  
QY 1058 TTCGGAGGCTTGATTTACCATGTTGACACCATTTGTCGGCGACCTTCCTTCGCCACAAC 1117  
Db 1252 ACTGGGGGACTCGACACCCAGATTGAGCATGACCTGTTTCCACAAATGCCAGGCACAAC 1311  
QY 1118 CTGACAGCGGTTAGCTACCAAGTGGGAACAGCTGTGCCAGAAAGCAACACCTGCCGTA 1173  
Db 1312 TACCCCAAGATCGCACCTCAGTTCGAGGCTCTTTGCAAGAACAGCGCCTCGAGTA 1367

## RESULT 12

AAF25729

ID AAF25729 standard; DNA; 2040 BP.

XX

AC AAF25729;

XX

DT 06-APR-2001 (first entry)

XX

C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.

XX

Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;

KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;

KW cosmetic; ds.

XX

OS Ceratodon purpureus.

XX

FH Key Location/Qualifiers

FT CDS 176..1627

FT /tag= a

FT /product= "delta6-acetylenase/delta6-desaturase"

FT

XX

PN WO200075341-A1.

XX

PD 14-DEC-2000.

XX

PF 07-JUN-2000; 2000WO-EP05274.

XX

PR 07-JUN-1999; 99DE-1025718.

XX

PR 22-DEC-1999; 99DE-1062409.

XX

PA (BADI ) BASF AG.

XX

PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaeheringer U;

XX

DR WPI; 2001-112150/12.

DR P-PSDB; AAB46435.

XX

Nucleic acid encoding delta6-acetylenase or desaturase, useful for

PT producing plant oils with increased content of unsaturated fatty acids

PT

XX

PS Claim 1a; Page 41-44; 69pp; German.

XX

This invention describes a novel isolated nucleic acid (I) encoding

CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase

CC activity. The invention also describes (a) amino acid sequences encoded

CC by (I); (b) an expression cassette (EC) containing (I) linked to one or  
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)  
CC organisms containing (I), EC or the vectors of (c); (e) preparation of  
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content  
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)  
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)  
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by  
CC method (g). (I) are used to produce transgenic plants (or other  
CC organisms) that produce oils or triglycerides (TG) with increased content  
CC of unsaturated fatty acids (A) and to isolate related sequences by  
CC homolog screening. (A), or TG containing them, are useful in human  
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and  
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,  
CC can be used to suppress expression of (II), resulting in oils with  
CC increased content of saturated fatty acids.

SQ Sequence 2040 BP; 528 A; 450 C; 505 G; 557 T; 0 other;

Query Match 5.6%; Score 71.6; DB 22; Length 2040;

Best Local Similarity 45.4%; Pred. No. 3.5e-11;

Matches 352; Conservative 0; Mismatches 409; Indels 15; Gaps 2;

QY 401 TTGCTTGGGATGCACTATCAACAGATGGCTGGCTTCTCATGACATTTGCCACCACAG 460

Db 770 TTGATGGGCTCTTCGTCCAAACAGTGTGGTGTGCCCATGATTCCTTCATCAACAG 829

QY 461 ACTTTTCAAGAACCCGGAACCTCGTGGGACTGGTATTTGGCAATGGTCTGCAA 520

Db 830 GTCTTTGAGAACCGTACCGCACTCTCTTCTTGCTATTTGTCGGCAATTCGCTGCTT 889

QY 521 GGTGTTTCCGTCATGTTGGAAGACAGACACATGACATTCATTCGGCAACCAATGTT 580

Db 890 GGCCTTAGTGTATCATGTGTGGAGGACGAACACACATTCATCATCTGCTCCGAATGAG 949

QY 581 CAAGGACGACGACCTGATATTGACAACCTCCCTCCCTTGGCTGTGCTGAGGATCAGCTC 640

Db 950 TGGCAGCAACAGTACACACCTCTAGACGAAGACATGTGATCTCTCCCATCATTCGCTGG 1009

QY 641 ACAGCGCGCTCACCGATTTCCCGCAAGCTCATTCAGTTCCAGCAGTACTATTTCCTTGGTC 700

Db 1010 AGCAAGGAATTTTGGCCACCGTTGAGAGCAAGAGAAATTTCCGAGTCTTCAATATCAG 1069

QY 701 ATCTGTATCTTGTTCGGGTTTCATTTGGTGTTCAGTCCGCTGTTGACCGTGGCAGTTTG 760

Db 1070 CACTACATGATTCCTGCTCTATTGTTATGTCGCGGTACAGTTGGACTTTTGGAAAGTTG 1129

QY 761 AAGGACAGAGATACCAATTCATCGCT--CTCAGTATAAGAGAGGCCATTCGCTC 817

Db 1130 CTCTTCATTCATCTCTGATTTGAGCAGCAGCAAGGATTTGATAGAAAGGGAACAGTT 1189

QY 818 GCCCTGCACCTGGACCTTGAAGGCCCTGTTCCACTTATTTCTTTATGCCCAGCATCTCACA 877

Db 1190 GCTTTTCACTACGCTGTTGAGTTCAGTTGGCTGCTTCCATATTTTGGCGGCTCTCGCTAAG 1249

QY 878 TCGCTGTTGTTGTTTTCGTTTCGGAGCTGTTGGCGGCTTCGGCATTCGATTCGTTG 937

Db 1250 CCTCTTGGTGGATGGTAGCAACTGAGCTTGTGCGCGGTTTGTGTTGGGATTCGCTGTT 1309

QY 938 TTCTATGAACCACTACCCACTGGAGAAGATCGGGGACCCAGTCTGGGATGGCCATGGATTC 997

Db 1310 ACCTTGAGTCACAAATGGAAGAGGTTTACAAATGAATCG-----AAGACTTC 1357

QY 998 TCGGTTGGCCAGATCCCATGAGACCATGAACATTCGGGAGGAGGATTTATCAGATTTGGTTT 1057

Db 1358 GTGAGACCCAGGTTATTACCCCGTAACACCAAGCGAGGCTGGTTCACAGATTGGTTTC 1417

QY 1058 TTGGAGGCTTGAATTACCAAGATTGAGCACCATTGTTGGCGGACCCCTCCCTCGCCACAAC 1117

Db 1418 ACTGGGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCACAAATGCCAGGCACAAC 1477

QY 1118 CTGACAGCGGTTAGCTACCAAGGTGGAACAGCTGTGCCAGAAAGCAACACCTGCCGTA 1173

Db 1478 TACCCCAAGATCGCACCTCAGGCTCTTTTGAAGAGCAGCGGCTCGAGTA 1533





Query Match 4.8%; Score 61.6; DB 21; Length 1934;  
 Best Local Similarity 57.1%; Pred. No. 4.3e-08;  
 Matches 112; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY	985	TGGCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATGAAACATTCGCGGAGGGATTAT	1044
Db	1336	TGGGAATGACTGGTTTGAGAAGCAGACAAAGTGTACATTGGATATCTCTGTGCCCTCTTC	1395
QY	1045	CACAGATTGGTTTTCGGGAGGCTTGAATTACCAGATTGAGCACCATTTGTGGCCGACCT	1104
Db	1396	GATGGATTGGTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTGTTCCAGGCT	1455
QY	1105	CCCTGCCACAAACCTGACAGCGTTAGCTACAGGTGGAACAGCTGTGCCAGAAGCACAA	1164
Db	1456	ACCTCGTGCCCAATTGAGGAAGATTTCGCCCTTGGTTAGTGACCTTTCGAAGAAGCATAA	1515
QY	1165	CCTGCCGTATCGGAAC	1180
Db	1516	TTTGCTTATAGGAGC	1531

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 Job time : 316.464 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:22:56 ; Search time 64.7752 Seconds  
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Perfect score: 1275

Sequence: 1 attttttcgaatgaagt.....gcgggggaaggctctataagg 1275

Scoring table: IDENTITY\_NUC

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121.6	9.5	1617	2	US-08-834-655-1
2	121.6	9.5	1617	3	US-08-834-033A-1
3	121.6	9.5	1617	3	US-09-363-574-1
4	121.6	9.5	1617	4	US-09-383-526-1
5	121.6	9.5	1617	4	US-09-330-235-17
6	51.8	4.1	1684	2	US-08-831-570-1
7	51.8	4.1	1684	2	US-08-831-575-1
8	51.8	4.1	1685	1	US-08-366-779-4
9	51.8	4.1	1685	1	US-08-789-936-4
10	51.8	4.1	1685	4	US-08-934-254-4
11	51	4.0	1686	4	US-09-439-261-6
12	51	4.0	1686	4	US-09-227-613-6
13	51	4.0	1843	4	US-09-439-261-7
14	51	4.0	1843	4	US-09-227-613-7
15	51	4.0	2257	4	US-09-439-261-8
16	51	4.0	2257	4	US-09-227-613-8
17	48.4	3.8	449	4	US-09-439-261-38
18	48.4	3.8	449	4	US-09-227-613-37
19	48.4	3.8	655	4	US-09-439-261-3
20	48.4	3.8	655	4	US-09-227-613-3
21	48.4	3.8	864	4	US-09-439-261-12
22	48.4	3.8	864	4	US-09-227-613-13
23	47.6	3.7	1702	4	US-08-934-254-26
24	45.6	3.6	473	4	US-09-439-261-37
25	45.6	3.6	473	4	US-09-227-613-36
26	45.6	3.6	1335	4	US-09-439-261-1
27	45.6	3.6	1335	4	US-09-227-613-1

28 44.8 3.5 918 4 US-09-439-261-5 Sequence 5, Appl  
29 44.8 3.5 918 4 US-09-227-613-5 Sequence 5, Appl  
30 44.8 3.5 960 4 US-09-439-261-36 Sequence 36, Appl  
31 44.8 3.5 960 4 US-09-227-613-35 Sequence 35, Appl  
32 44.8 3.5 990 4 US-09-439-261-35 Sequence 35, Appl  
33 44.8 3.5 990 4 US-09-227-613-34 Sequence 34, Appl  
34 41 3.2 6344 4 US-08-843-417-1 Sequence 1, Appl  
35 41 3.2 6524 4 US-08-669-656A-1 Sequence 1, Appl  
36 41 3.2 6527 4 US-08-669-656A-7 Sequence 7, Appl  
37 41 3.2 7052 4 US-08-669-656A-5 Sequence 5, Appl  
38 39.2 3.1 7218 1 US-08-232-463-14 Sequence 14, Appl  
39 35 2.7 428 4 US-09-397-787-246 Sequence 246, Appl  
40 33.8 2.7 4403765 4 US-09-103-840A-2 Sequence 2, Appl  
41 33.8 2.7 4411529 4 US-09-103-840A-1 Sequence 1, Appl  
42 33.6 2.6 2997 1 US-08-453-862-1 Sequence 1, Appl  
43 33.6 2.6 2997 2 US-08-452-734A-1 Sequence 1, Appl  
44 33.6 2.6 2997 4 US-08-176-401B-1 Sequence 1, Appl  
45 33.6 2.6 2997 5 PCT-US94-14989-1 Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-834-655-1  
; Sequence 1, Application US/08834655  
; Patent No. 5968809  
; GENERAL INFORMATION:  
; APPLICANT: KNUITZON, DEBORAH  
; APPLICANT: MURKERJI, PRADIP  
; APPLICANT: HUANG, YUNG-SHENG  
; APPLICANT: THURMOND, JENNIFER  
; APPLICANT: CHAUDHARY, SUNITA  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS  
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.  
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,655  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RAE-VENTER, BARBARA  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: CGNE.124.00US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 328-4400  
TELEFAX: (650) 328-4477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-834-655-1

Query Match 9.5%; Score 121.6; DB 2; Length 1617;  
Best Local Similarity 49.3%; Pred. No. 1.8e-28;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

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QY 394 GGCAGTGTTCCTGGGATGACATATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453
Db 538 GGCCTGGCTTTTGGGCTGTCTTGGCAGCAGTCCGGATGGTGGCTCAACGACTTTTGGCA 597
QY 454 CCACCAAGACTTTCAAGAACCGGAACATGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513
Db 598 TCACCAAGTCTTCCAGACCGTTCTGGGGTGATCTTTCGGGCGCTTCTTGGGAGGTGT 657
QY 514 TCTGCAAGGTTTTTCCGTCGATGTTGGGAAGGACAGACAAATGACATCATTTCCGGAAC 573
Db 658 CTGCCAGGCTTCTCGCTCTGCTGGTGAAGGACAAACACATCACCACCGCCGCC 717
QY 574 CAATGTTCAAGGACAGACCTCATATGACACCTCCGCCCTTAGCCTGGTCTGAGGA 633
Db 718 CACGTCACCGGAGGATCCCGACATGACACCCACCTCTCTGACCTGGAGTGAGCA 777
QY 634 T-----GACGTCACACGGGCGTCAACCGATTTCCCGCAA 666
Db 778 TGGCTTGGAGATGTTCTCGGATGTCACAGATGAGGAGCTGACCCGATGTGGTCCGCTTT 837
QY 667 GCTCATTCAGTTCACAGACTATTTCTGGTCTGATCTGTATCTTGTTCGGGTTCATTTG 726
Db 838 CATGGTCTTCAACAGACCTGGTTTACTTCCCACTTCTCTCGTTTGGCCCTCTCTCTG 897
QY 727 GTGTTTCCAGTGGCTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAAT 780
Db 898 GTCCCTCCAGTCCATTTCTTGTGCTGCTTAACGGTCAAGGCGGACCAAGCCCTCGGGCGC 957
QY 781 CTATCGCTCTCAGTATAAAGAGGAGGCGCATTTGGCCTCGCCTGCATCGACCTTGAAGGC 840
Db 958 GCGTGTGCCATCTCGTTTGGTCCAGAGCTGTGCTTGGCATGCACTGGACCTGGTACCT 1017
QY 841 CTTGTTCCACTTATCTTTATGCCCCAGCATCTGATCTGATCTGTTGGGTTTCAATTTG 900
Db 1018 CGCCACCATGTTCTCTTTCATCAAGGATCCCGTCAACATGCTGCTGATCTTTTGGTGT 1077
QY 901 GGAGCTGTTGGGGCTTCCGCAATTCGATCGTGGTTCATCAACACCTACCCACTGGA 960
Db 1078 GCAGGCGGTGGCGAACTGTTGGGATCGTGTCTCGCTCAACCAACAGGATGACC 1137
QY 961 GAAGATGGGGACCCAGTCTGGGATGGCCATGATTTCTCGTTTGGCCATCCATGAGAC 1020
Db 1138 TGTGATCTCGAAGGAGGAGCGCTCGATATGATTTCTTCAACGACGATCATCAGGG 1197
QY 1021 CATGAACATTCGGCGAGGATTAACAGATTCGTTTTCGGAGGCTTGAATTAACAGAT 1080
Db 1198 TCGTGTATGCCACCGGGTCTATTGGCAACTGTTTACGGGTGATTTGAACATATCAGAT 1257
QY 1081 TGAGCACCATTTCTGTCGCGACCTTCCCTCGCCCAACCTGACAGCGGTAGCTACCAGGT 1140
Db 1258 CGAGCACCATTTCTTCCCTTGGATGCTTCCCAACTTTTCAAGATCCAGCGCTGCTGT 1317
QY 1141 GGAACAGCTGTGCGAAGCACACCTTCCGCTATCGGAACC 1182
Db 1318 CGAGACCTGTGCAAAAGTACATGTCCGATACCACACCAC 1359
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## RESULT 2

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US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
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; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-033A-1
;
; Query Match 9.5% Score 121.6; DB 3; Length 1617;
; Best Local Similarity 49.3%; Pred. No. 1.8e-28;
; Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;
;
; QY 394 GGCAGTGTTCCTGGGATGACATATCAACAGATGGCTGGCTTCTCATGACATTTGCCA 453
; Db 538 GGCCTGGCTTTTGGGCTGTCTTGGCAGCAGTCCGGATGGTGGCTCAACGACTTTTGGCA 597
; QY 454 CCACCAAGACTTTCAAGAACCGGAACATGGAACACCTCGTGGGACTGGTATTTGGCAATGG 513
; Db 598 TCACCAAGTCTTCCAGACCGTTCTGGGGTGATCTTTCGGGCGCTTCTTGGGAGGTGT 657
; QY 514 TCTGCAAGTGTTCCTGGATGATTTGGAAGGACAGACAAATGACATCATTTCCGGAAC 573
; Db 658 CTGCCAGGCTTCTCGCTCTGCTGGTGAAGGACAAACACATCACCACCGCGGCC 717
; QY 574 CAATGTTCAAGGACAGACCTCATATGACACCTCCGCCCTTAGCCTGGTCTGAGGA 633
; Db 718 CACGTCACCGGAGGATCCCGACATGACACCCACCTCTCTGTTGACCTGGAGTGAGCA 777
; QY 634 T-----GACGTCACACGGGCGTCAACCGATTTCCCGCAA 666
; Db 778 TGGCTTGGAGATGTTCTCGGATGTCACAGATGAGGAGCTGACCCGATGTGGTCCGCTTT 837
; QY 667 GCTCATTCAGTTCACAGACTATTTCTGGTCTGATCTGTATCTTGTTCGGGTTCATTTG 726
; Db 838 CATGGTCTTCAACAGACCTGGTTTACTTCCCACTTCTCTCGTTTGGCCCTCTCTCTG 897
; QY 727 GTGTTTCCAGTGGCTGTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAAT 780
; Db 898 GTCCCTCCAGTCCATTTCTTGTGCTGCTTAACGGTCAAGGCGGACCAAGCCCTCGGGCGC 957
; QY 781 CTATCGCTCTCAGTATAAAGAGGAGGCGCATTTGGCCTCGCCTGCATCGACCTTGAAGGC 840
; Db 958 GCGTGTGCCATCTCGTTTGGTCCAGAGCTGTGCTTGGCATGCACTGGACCTGGTACCT 1017
; QY 841 CTTGTTCCACTTATCTTTATGCCCCAGCATCTGATCTGATCTGTTGGGTTTCAATTTG 900
; Db 1018 CGCCACCATGTTCTCTTTCATCAAGGATCCCGTCAACATGCTGCTGATCTTTTGGTGT 1077
; QY 901 GGAGCTGTTGGGGCTTCCGCAATTCGATCGTGGTTCATCAACACCTACCCACTGGA 960
; Db 1078 GCAGGCGGTGGCGAACTGTTGGGATCGTGTCTCGCTCAACCAACAGGATGACC 1137
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QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATGGATTCTCGGTTGCCAGATCCATGAGAC 1020  
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Db 1198 TCGTATGTCACCGCGGTCTATTGGCAACTGGTTTCACGGGTGGATTGAACATATCAGAT 1257  
QY 1081 TGACACCATTTGGCCGACCCCTCCCTCGCCACAACTGACAGCGGTTAGCTACCAAGT 1140  
Db 1258 CGAGACCATTTGTTCCCTTCGATGCTTCGACCAAACTTTTCAAGATCCAGCCTGCTGT 1317  
QY 1141 GGAACAGCTGTCGAGAGCAGCAACTGCCGTATCGGAACCC 1182  
Db 1318 CGAGACCTGTGCAAAAAGTACATGTCGGATACCAACCAC 1359

## RESULT 3

US-09-363-574-1

; Sequence 1, Application US/09363574

; Patent No. 6136574

; GENERAL INFORMATION:

; APPLICANT: KNUTZON, DEBORAH

; APPLICANT: MURKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/363,574

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-202 USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1617 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

US-09-363-574-1

Query Match

Best Local Similarity 9.5%; Score 121.6; DB 3; Length 1617;

Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

QY 394 GGCAGTGTGCTGGGATGCACTATCAACAGATGGGTGCTTCTCATGACATTTGCCA 453

Db 538 GGCTGCGCTTTGGTCTGTTCTGGCAGCAGTGGTGTGGCTCAGCACTTTTGCA 597

QY 454 CCACCAGACTTTCAGAACCGGAACCTCTGTGGGACTGGTATTGTCGAATGG 513

Db 598 TCACAGGTCTTCAGGACCGTTCGCGGTGATCTTTTCGCGCCCTCTTTCGGAGGTGT 657  
QY 514 TCTCAAGTCTTTTCGTCGACATGTTGGAAGCAGACACAATGCAATATTCGGAAC 573  
Db 658 CTGCCAGGCTTCTCGTCTCGTGGTGAAGCAAGCAACACTCACCACGCCGCC 717  
QY 574 CAATCTTCAAGGCGACGACCTGATATGACAACCTCCCTTACCTAGCTGGTCTGGA 633  
Db 718 CAACGTCCAGCGGAGGATCCCGACATTCACACCCACCTCTGTTCACCTGGAGTGAGCA 777  
QY 634 T-----GACGTCACACGGGGGTTCACCGGATTTCCCGCAA 666  
Db 778 TCCGTTGGAGATGTTCTCGGATGTCAGATGAGGAGCTGACCCGATGTGGTCGGTTT 837  
QY 667 GCTATTGAGTTCAGCAGTACTATTTCTTGTGTCATCTGTATCTTGTGGGTTCATTTG 746  
Db 838 CATGCTCTGAACACGACCTGCTGTTTACTTCCCACTCTCTGTTTTCGCGCTCTCTCTG 897  
QY 727 GTGTTTCCAGTCCGTTGACCGTGC-----GCAGTTTGAAGGACAGAGATAACCAATT 780  
Db 898 GTGCTCCAGTCCATCTCTTGTGCTGCTTAACGGTCAAGGCTCAGGCCCAAGCCCTCGGGCGC 957  
QY 781 CTATGCTCTCAGTATAAGAGGAGGCCATTTGCCCTCGCCCTGCACTGGACCTTGAAGGC 840  
Db 958 CGGTGCGCCATCTCGTTGGTCGACGAGCTGTCGCTTGGATGCACTGGACCTGGTACCT 1017  
QY 841 CCTGTTCCACTTATTTTATGCCAGCATCTCATACGCTGTTGGTGTGTTTTCGTTTC 900  
Db 1018 CGCCACCATGTTCTCTTTCATCAAGGATCCCGCTCAACATGCTGTTGTTGTTGTTGTC 1077  
QY 901 GGAGCTGTTGGCGCTTCGGCATTTGCGATGCTGTTGTTTCATGAACCACTACCACTGGA 960  
Db 1078 CGAGCGGTGTCGGAAACTTGTGGCGATGCTGTTCTCGCTCAACCAACGATATGCC 1137  
QY 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGCTCGTTGGCAGATCCATCAGAC 1020  
Db 1138 TGTGATCTCGAAGGAGGAGGCGGTGATATGATTTCTTCAGNAGCAGATCATCACGG 1197  
QY 1021 CATGAACATTCGGGAGGAGGATATCAGATTTGGTTTTTCGGAGGCTTGAATACAGAT 1080  
Db 1198 TCGTATGTCACCGCGGTCTATTTCGCAACTGTTTTCAGGGTGGATTGAACATATCAGAT 1257  
QY 1081 TGAGCACCATTTTGGCGGACCCCTCCCTCGCCACAACTGACAGCGGTTAGCTACCAAGT 1140  
Db 1258 CGAGCACCATTTGTTCCCTTCGATGCTCGCCACAACTTTTCAAGATCCAGCCTGCTGT 1317  
QY 1141 GGAACAGCTGTCGAGAGCAGCAACTGCCGTATCGGAACCC 1182  
Db 1318 CGAGACCTGTGCAAAAAGTACATGTCGGATACCAACCAC 1359

## RESULT 4

US-09-363-526-1

; Sequence 1, Application US/09363526

; Patent No. 6410288

; GENERAL INFORMATION:

; APPLICANT: KNUTZON, DEBORAH

; APPLICANT: MURKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,526  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WARD, MICHAEL R.  
REGISTRATION NUMBER: 38,651  
REFERENCE/DOCKET NUMBER: CGAB-201 USA  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: N/A

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1617 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-09-363-526-1

Query Match 9.5%; Score 121.6; DB 4; Length 1617;

Best Local Similarity 49.3%; Pred. No. 1.8e-28;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

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QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGGTGGCTTCTCATGACATTTGGCA 453
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Db 538 GGTGGCTTTTGGTCTGTCTGGCAGCAGTGGGATGTTGGCTCAGCAGTCTTTGCA 597

QY 454 CCACGAGCTTCAAGAACCGGACCTGGAACACCTCGTGGGACTGGTATTTGGCAATG 513
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Db 658 CTGCCAGGGCTTCCTGCTCTGTTGGTGAAGGACAGACAACACTACACACGCGCC 717

QY 574 CAATGTTCAAGGACGACGCTGATATTGACACCTCCCCCTTAGCCTGGTCTGAGGA 633
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Db 718 CAACGTCCACGGGAGGATCCGACATTTGACACCCCTCTGTGACCTGGAGTGAGCA 777

QY 634 T-----GAGCTCACACGGCGTCCACCGATTTCCCGCAA 666
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Db 778 TCGTGTGGAGATGTTCTCGGATGCCAGATGAGGAGCTGACCCGCACTGTCGCGTT 837

QY 667 GCTCATTCAGTTCAGCAGTACTATTTCTGGTATCTGTGATCTGTGTCGGTTCATTG 726
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 CATGGTCTGAAACAGACCTGTTTACTTCCCATCTCTCGTTGCCCGCTCTCTCTG 897

QY 727 GTGTTTCCAGTGGTGTGACCGTGC-----GAGTTTGAAGGACAGAGATAACCAATT 780
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Db 898 GTCCCTCCAGTCCATTCTCTTGTGCTGCTTAACGGTACAGGCCCAACAGCCCTCGGCGC 957

QY 781 CTATCGCTCTCAGTATGAAGAGGAGGCAATTTGGCTCGCCCTGCACCTGGACCTGAAGGC 840
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Db 1078 GCAGGCGGTGTGGGAACATTGTGGGATCTGTCTCTGCTCAACCAACAGGATGCC 1137

QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATCGGATTTGGGCAATCCATGAGAC 1020
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Db 1138 TGTGATCTCAAGGAGGCGGTGCGATATGGATTTCTTCCAGGAAGCAGATCATCAGGG 1197
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QY 1021 CATGAACATTCCGGAGGATTATCACAGATTTGTTTTTCGGAGGCTTGAATTACCAGAT 1080
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Db 1198 TCGTGTATGCCACCGGCTATTTGCAACTGGTTCACGGTGTGAATGAACTATCAGAT 1257

QY 1081 TGAGCACCAATTTGTGGCCGACCTCCCTCCGCCAACCTGACAGCGGTGTAGCTACCAGGT 1140
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Db 1258 CGAGCACCACTTGTTCCTTCGATGCCCTCGCCACAACTTTTCAAAGATCCAGCCTGCTGT 1317

QY 1141 GGAACAGCTGTGCCAGAGACACACCTGCGGTATCGGAACCC 1182
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Db 1318 CGAGACCTGTGCAAAAATACAAATGTCCGATACCAACACCAC 1359
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## RESULT 5

US-09-330-235-17  
; Sequence 17, Application US/09330235  
; Patent No. 6459018  
; GENERAL INFORMATION:  
; APPLICANT: Knutzon, Debbie  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS  
; FILE REFERENCE: MOCO.156.00US  
; CURRENT APPLICATION NUMBER: US/09/330.235  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: 60/089,043  
; PRIOR FILING DATE: 1998-06-12  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Mortierella alpina  
US-09-330-235-17

Query Match 9.5%; Score 121.6; DB 4; Length 1617;

Best Local Similarity 49.3%; Pred. No. 1.8e-28;  
Matches 405; Conservative 0; Mismatches 384; Indels 33; Gaps 2;

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QY 394 GGCAGTGTTCCTGGGATGCACATCAACAGATGGGTGGCTTCTCATGACATTTGGCA 453
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Db 538 GGTGGCTTTTGGTCTGTCTGGCAGCAGTGGGATGTTGGCTCAGCAGTCTTTGCA 597

QY 454 CCACGAGCTTCAAGAACCGGACCTGGAACACCTCGTGGGACTGGTATTTGGCAATG 513
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Db 598 TCACAGGTCTTCAGGACCGTCTTGGGTGATCTTTTCGGCGCTTCTTGGGAGGTG 657

QY 514 TCTGCAAGGTTTTTCCGTGACATGTTGGAAGGACAGACAATGCACATCATTCGGCAAC 573
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 CTGCCAGGGCTTCCTGCTCTGTTGGTGAAGGACAGACAACACTACACGCGCC 717

QY 574 CAATGTTCAAGGACGACGCTGATATTGACACCTCCCCCTTAGCCTGGTCTGAGGA 633
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Db 778 TCGTGTGGAGATGTTCTCGGATGCCAGATGAGGAGCTGACCCGCACTGTCGCGTT 837

QY 667 GCTCATTCAGTTCAGCAGTACTATTTCTGGTATCTGTGATCTGTGTCGGTTCATTG 726
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Db 838 CATGGTCTGAAACAGACCTGTTTACTTCCCATCTCTCGTTGCCCGCTCTCTCTG 897

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Db 898 GTCCCTCCAGTCCATTCTCTTGTGCTGCTTAACGGTACAGGCCCAACAGCCCTCGGCGC 957

QY 781 CTATCGCTCTCAGTATGAAGAGGAGGCAATTTGGCTCGCCCTGCACCTGGACCTGAAGGC 840
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Db 958 GCAGGCGGTGTGGGAACATTGTGGGATCTGTCTCTGCTCAACCAACAGGATGCC 1017

QY 841 CTGTTTCCAGTGGTGTGACCGTGC-----GAGTTTGAAGGACAGAGATAACCAATT 780
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Db 998 GTCCCTCCAGTCCATTCTCTTGTGCTGCTTAACGGTACAGGCCCAACAGCCCTCGGCGC 957

QY 781 CTATCGCTCTCAGTATGAAGAGGAGGCAATTTGGCTCGCCCTGCACCTGGACCTGAAGGC 840
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Db 958 GCAGGCGGTGTGGGAACATTGTGGGATCTGTCTCTGCTCAACCAACAGGATGCC 1017

QY 841 CTGTTTCCAGTGGTGTGACCGTGC-----GAGTTTGAAGGACAGAGATAACCAATT 780
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Db 998 GTCCCTCCAGTCCATTCTCTTGTGCTGCTTAACGGTACAGGCCCAACAGCCCTCGGCGC 957

QY 781 CTATCGCTCTCAGTATGAAGAGGAGGCAATTTGGCTCGCCCTGCACCTGGACCTGAAGGC 840
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Db 958 GCAGGCGGTGTGGGAACATTGTGGGATCTGTCTCTGCTCAACCAACAGGATGCC 1017

QY 961 GAAGATCGGGACCCAGTCTGGGATGGCCATCGGATTTGGGCAATCCATGAGAC 1020
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1018 CGCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATGCTGGTGTACTTTTGGTGTG 1077
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,254  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 83832XWVU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1685 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-934-254-4

Query Match 4.1%; Score 51.8; DB 4; Length 1685;  
Best Local Similarity 56.9%; Pred. No. 3e-06;  
Matches 95; Conservative 0; Mismatches 72; Indels 0; Gaps 0;  
QY 1007 CAGATCCATGACACCATTCGGCGGAGGATTATACAGATGCTGTTTCGGAGGC 1066  
DB 1091 CAACCGATGGGACACTTGACATTTCTGTCTCTCTGGATGGATTGTTTCATGGTGA 1150  
QY 1067 TTGAATACAGATTGACGACCATTTGTGGCGGACCTCCCTCGCCACAACTGACAGCG 1126  
DB 1151 TTGCAATTCGAATGAGCATCTTTTCCCAAGATGCTAGATGCAACCTTAGGAAA 1210  
QY 1127 GTTAGTACAGGTGGACAGCTGTGCCAGAACACAACTGCGGTA 1173  
DB 1211 ATCTGCGCTACGTGATGAGTATGCAAGAAACATAATTTGCTTA 1257

RESULT 11  
US-09-439-261-6  
Sequence 6, Application US/09439261  
Patent No. 6428990  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.P2  
CURRENT APPLICATION NUMBER: US/09/439,261  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 1686  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-439-261-6

Query Match 4.0%; Score 51; DB 4; Length 1686;  
Best Local Similarity 46.7%; Pred. No. 5.4e-06;  
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGCCATTGGCCTCGCCCTGCACCTGAGACCTTGAAGGCCCTGTTCAC 850  
DB 261 CATAAGAACTGGGTGGACCTGGCCTGGGCCCTAGCTACTACATCCGGTCTTTCATCAC 320  
QY 851 TTATTCTTTATGCCAGCATCCTCACATCGCTGTTGGTGTGTTTTCGTTTCGGAGCTGGT 910  
DB 321 TACATCCCTTTCTAGGGCATCTCGGAGCCCTCTCTTTCCTCAACTTATCAGGTTCCTG 380  
QY 911 GCGGCTTCGGCATTCGGATCGTGTTCATGAACCACTACCCACTGGAGAGATCGGG 970  
DB 381 GAGAGCCACTGGTGTGTTGGTTCACAGATGAATCATCATCGTTCATGAGATTGACCAG 440  
QY 971 GACCCAGTCTGGGATGGCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATGAACATT 1030  
DB 441 GA-----GGCCTACCGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACGCTG 491  
QY 1031 CGGCGAGGATTATACAGATTTGTTTTCGGAGGCTTGAATTACAGATTGAGCACCATT 1090  
DB 492 GAGCAGTCTTCTTCAAGCACTGTTTCTAGTGGACACCTTAATCTCCAGATTGAGCACC 551  
QY 1091 TTGTGGCGGACCTCTCTCGCCACAACTGACAGCGTTAGCTACCAAGTGGAGAGCTG 1150  
DB 552 CTCTTCCCACTGCGCCGACAACTTACACAAAGATCGCCCGCTGGTGAAGTCTCTA 611  
QY 1151 TGCAGAGAACAACTGCGCTATCGGNAACCGCTGCCCCATGAAGGTTGGTCACTCTG 1210  
DB 612 TGTCCCAAGCATGTCATTGAATACAGGAGAGCGCTACTGAGGCGCTGCTGGACATC 671  
QY 1211 CTGCGCTATCTGGCGGTGT 1229  
DB 672 ATCAGGTCCTTGAAGAAGT 690

RESULT 12  
US-09-227-613-6  
Sequence 6, Application US/09227613A  
Patent No. 6432684  
GENERAL INFORMATION:  
APPLICANT: MUKERJI, Pardip  
APPLICANT: LEONARD, Amanda E.  
APPLICANT: HUANG, Yung-Sheng  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.P1  
CURRENT APPLICATION NUMBER: US/09/227,613A  
CURRENT FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 1686  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-227-613-6

Query Match 4.0%; Score 51; DB 4; Length 1686;  
Best Local Similarity 46.7%; Pred. No. 5.4e-06;  
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGCCATTGGCCTCGCCCTGCACCTGAGACCTTGAAGGCCCTGTTCAC 850  
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QY 851 TTATTCTTTATGCCAGCATCCTCACATCGCTGTTGGTGTGTTTTCGTTTCGGAGCTGGT 910  
DB 321 TACATCCCTTTCTAGGGCATCTCGGAGCCCTCTCTTTCCTCAACTTATCAGGTTCCTG 380  
QY 911 GCGGCTTCGGCATTCGGATCGTGTTCATGAACCACTACCCACTGGAGAGATCGGG 970  
DB 381 GAGAGCCACTGGTGTGTTGGTTCACAGATGAATCATCATCGTTCATGAGATTGACCAG 440  
QY 971 GACCCAGTCTGGGATGCCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATGAACATT 1030

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QY 1151 TCCCAAGACCAACCTGCGGTATCGGAACCGCTGCCCCATGAAGGTTGGTCAATCTG 1210  
Db 612 TGTGCCAAGCATGGCATTAATACCAAGGAGAGCCGCTACTAGGSCCCTGCTGGACATC 671  
QY 1211 CTGCGCTATCTGGCGGTGT 1229  
Db 672 ATCAGGTCCCTGAAGAAGT 690

## RESULT 13

US-09-439-261-7

; Sequence 7, Application US/09439261

; Patent No. 6428990

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pradip

; APPLICANT: Leonard, Amanda E.

; APPLICANT: Huang, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295.US.P2

; CURRENT APPLICATION NUMBER: US/09/439,261

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: US 08/833,610

; PRIOR FILING DATE: 1997-04-11

; PRIOR APPLICATION NUMBER: PCT/US98/07422

; PRIOR FILING DATE: 1998-04-10

; PRIOR APPLICATION NUMBER: US 09/227,613

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-261-7

Query Match 4.0%; Score 51; DB 4; Length 1843;

Best Local Similarity 46.7%; Pred. No. 5.7e-06;

Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGCCATTTGCCCTCGCCCTGCACTGGACCTTGAAGGCCCTGTTCCAC 850  
Db 418 CATAAGAACTGGTGGACCTGGCCCTGGCCGTCAGCTACTACATCCGGTTCTTCATCAC 477  
QY 851 TTATTTCTTTATGCCAGCATCTCACATCGCTGTTGGTGTTCCTTTCGGAGCTGGT 910  
Db 478 TACATCCCTTTTACGGCATCTCTGAGGCCCTCTTTTCTCAACTTCATCAGGTTCC 537  
QY 911 GCGCGGCTCGGCATTCGGATTCGGTGTTCATGAACCACTTACCCTGGAGAGATCGGG 970  
Db 538 GAGAGCCATGGTTGTGGTGCACACAGATGAATACATCTCATGAGATTGACCA 597  
QY 971 GACCCAGTCTGGATGGCCATGGATTCTCGGTTGGCCAGTCCATCCATGAGACCATTA 1030  
Db 598 GA-----GGCCTACCGTACTGTTTTCAGTAGCCAGCTGACAGCCACCTGCAACG 648  
QY 1031 CGCGGAGGATATACAGATTGGTTTTCGGAGGCTTGAATTACCAGATTGAGCAACAT 1090  
Db 649 GAGCAGTCTCTTCAACGACTGGTTTCAGTGGACACCTTAACCTCCAGATTGAGCA 708  
QY 1091 TTGTGGCCGACCTCCCTCGCCACAACCTGACAGCGGTTAGTACCAGGTTGGTCAAT 1150  
Db 598 GA-----GGCCTACCGTACTGTTTTCAGTAGCCAGCTGACAGCCACCTGCAACG 648  
QY 1031 CGCGGAGGATATACAGATTGGTTTTCGGAGGCTTGAATTACCAGATTGAGCAACAT 1090  
Db 649 GAGCAGTCTCTTCAACGACTGGTTTCAGTGGACACCTTAACCTCCAGATTGAGCA 708  
QY 1091 TTGTGGCCGACCTCCCTCGCCACAACCTGACAGCGGTTAGTACCAGGTTGGTCAAT 1150

Db 709 CTCTTCCCAACCATGCCCCGGCACAACCTTACACAAGATGCCCCCGCTGGTGAAGTCTCTA 768  
QY 1151 TCCCAAGACCAACCACTGCGGTATCGGAACCGCTGCCCCATGAAGGTTGGTCAATCTG 1210  
Db 769 TGTGCCAAGCATGGCATTAATACCAAGGAGAGCCGCTACTAGAGGCCCTGCTGGACATC 828  
QY 1211 CTGCGCTATCTGGCGGTGT 1229  
Db 829 ATCAGGTCCCTGAAGAAGT 847

## RESULT 14

US-09-227-613-7

; Sequence 7, Application US/09227613A

; Patent No. 6432684

; GENERAL INFORMATION:

; APPLICANT: MUKERJI, Pradip

; APPLICANT: LEONARD, Amanda E.

; APPLICANT: HUANG, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295.US.P1

; CURRENT APPLICATION NUMBER: US/09/227,613A

; CURRENT FILING DATE: 1999-01-08

; PRIOR APPLICATION NUMBER: 08/833,610

; PRIOR FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-227-613-7

Query Match

Best Local Similarity 46.7%; Pred. No. 5.7e-06;

Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;

QY 791 CAGTATAAGAGAGGCCATTTGCCCTCGCCCTGCACTGGACCTTGAAGGCCCTGTTCCAC 850  
Db 418 CATAAGAACTGGTGGACCTGGCCCTGGCCGTCAGCTACTACATCCGGTTCTTCATCAC 477  
QY 851 TTATTTCTTTATGCCAGCATCTCACATCGCTGTTGGTGTTCCTTTCGGAGCTGGT 910  
Db 478 TACATCCCTTTTACGGCATCTCTGAGGCCCTCTTTTCTCAACTTCATCAGGTTCC 537  
QY 911 GCGCGGCTCGGCATTCGGATTCGGTGTTCATGAACCACTTACCCTGGAGAGATCGGG 970  
Db 538 GAGAGCCATGGTTGTGGTGCACACAGATGAATACATCTCATGAGATTGACCA 597  
QY 971 GACCCAGTCTGGATGGCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATTA 1030  
Db 598 GA-----GGCCTACCGTACTGTTTTCAGTAGCCAGCTGACAGCCACCTGCAACG 648  
QY 1031 CGCGGAGGATATACAGATTGGTTTTCGGAGGCTTGAATTACCAGATTGAGCAACAT 1090  
Db 649 GAGCAGTCTCTTCAACGACTGGTTTCAGTGGACACCTTAACCTCCAGATTGAGCA 708  
QY 1091 TTGTGGCCGACCTCCCTCGCCACAACCTGACAGCGGTTAGTACCAGGTTGGTGAAC 1150  
Db 709 CTCTTCCCAACCATGCCCCGGCACAACCTTACACAAGATGCCCCGCTGGTGAAGTCTCTA 768  
QY 1151 TCCCAAGACCAACCACTGCGGTATCGGAACCGCTGCCCCATGAAGGTTGGTCAATCTG 1210  
Db 769 TGTGCCAAGCATGGCATTAATACCAAGGAGAGCCGCTACTAGAGGCCCTGCTGGACATC 828  
QY 1211 CTGCGCTATCTGGCGGTGT 1229  
Db 829 ATCAGGTCCCTGAAGAAGT 847

## RESULT 15

US-09-439-261-8

; Sequence 8, Application US/09439261





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: July 2, 2003, 15:38:56 ; Search time 216.694 Seconds  
(without alignments)  
9184.672 Million cell updates/sec

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Perfect score: 1275  
Sequence: 1 atttttttcgaatgaagt.....gcggggaagctctataagg 1275

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107.4	8.4	1380	9 US-09-967-477B-7	Sequence 7, Appli
C 2	56	4.4	480	10 US-09-924-035A-370	Sequence 370, App
C 3	56	4.4	657	10 US-09-770-149-494	Sequence 494, App
4	56	4.4	1350	9 US-09-938-842A-558	Sequence 558, App
5	51.8	4.1	1685	12 US-10-029-756-4	Sequence 4, Appli
6	51	4.0	1474	9 US-10-102-806-232	Sequence 232, App
7	51	4.0	1686	9 US-10-191-513A-6	Sequence 6, Appli
8	51	4.0	1843	9 US-10-191-513A-7	Sequence 7, Appli
9	51	4.0	2257	9 US-10-191-513A-8	Sequence 8, Appli
10	49.6	3.9	1059	9 US-10-156-761-1580	Sequence 1580, Ap
C 11	49.6	3.9	9025608	9 US-10-156-761-1	Sequence 1, Appli
12	48.6	3.8	1095	9 US-10-156-761-2285	Sequence 2285, Ap
13	48.4	3.8	449	9 US-10-191-513A-37	Sequence 37, Appli
14	48.4	3.8	655	9 US-10-191-513A-3	Sequence 3, Appli
15	48.4	3.8	864	9 US-10-191-513A-13	Sequence 13, Appli
16	48.4	3.8	1928	9 US-10-262-617-4	Sequence 4, Appli
C 17	48.4	3.8	1972	10 US-09-822-849A-485	Sequence 485, App
18	47.6	3.7	1702	12 US-10-029-756-26	Sequence 26, Appli
19	45.6	3.6	473	9 US-10-191-513A-36	Sequence 36, Appli

20	45.6	3.6	1335	9 US-10-191-513A-1	Sequence 1, Appli
21	45.2	3.5	1478	9 US-09-981-876-63	Sequence 63, Appli
22	45.2	3.5	1478	9 US-09-148-545-63	Sequence 63, Appli
23	45.2	3.5	1717	9 US-10-262-617-2	Sequence 2, Appli
24	44.8	3.5	918	9 US-10-191-513A-5	Sequence 5, Appli
25	44.8	3.5	960	9 US-10-191-513A-35	Sequence 35, Appli
26	44.8	3.5	990	9 US-10-191-513A-34	Sequence 34, Appli
27	44.2	3.5	2016	9 US-09-981-876-119	Sequence 119, App
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C 29	43.4	3.4	347	9 US-09-736-457-355	Sequence 355, App
C 30	43.4	3.4	347	9 US-09-902-941-355	Sequence 355, App
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C 32	43.4	3.4	347	9 US-09-849-626-355	Sequence 355, App
C 33	43.4	3.4	347	9 US-10-017-754-355	Sequence 355, App
C 34	43.4	3.4	347	9 US-10-040-862-4558	Sequence 4558, Ap
35	43	3.4	287	10 US-09-878-574-3260	Sequence 3260, Ap
36	41	3.2	6344	9 US-10-209-776-1	Sequence 1, Appli
37	38.4	3.0	1479	9 US-10-156-761-1811	Sequence 1, Appli
38	38.4	3.0	9025608	9 US-10-156-761-1	Sequence 1, Appli
39	37.8	3.0	263	10 US-09-878-574-9255	Sequence 9255, Ap
40	37.6	2.9	476	10 US-09-770-444-39	Sequence 39, Appli
C 41	37.6	2.9	653	9 US-10-123-155-438	Sequence 438, App
42	36.4	2.9	2040	9 US-10-156-761-1439	Sequence 1439, Ap
43	35.6	2.8	533	9 US-10-184-644-44	Sequence 44, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 7, Application US/09967477B  
; Patent No. US20020156254A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiao Qiu  
; APPLICANT: Haiping Hong  
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL  
; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: BNZ-001  
; CURRENT APPLICATION NUMBER: US/09/967,477B  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/236,303  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/297,562  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Thraustochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1380)  
US-09-967-477B-7

Query Match		8.4%	Score 107.4;	DB 9;	Length 1380;
Best Local Similarity		47.6%	Pred. No. 4.9e+25;		
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QY	311	TACTCATACAAATCAGCACACACACTGGGCGCTTGGAGTGT-----GGGTATTTC	361		
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QY 1055 TTTTTCGAGGCTTGAATACCAGATTGAGCACCATTGTTGGCGGACCTCCCTCGGCAC 1114
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DB 1228 AACTGCGCAAGGTACAGTGTCTCATCAAGTCGTATGCAAGAGTTCGACATCCCGTTC 1287
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## RESULT 2

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; Sequence 370, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Grlach, Jn
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 201105
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSEQ for Windows Version 3.0
```

```
; SEQ ID NO 370
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-924-035A-370

Query Match 4.4%; Score 56; DB 10; Length 480;
Best Local Similarity 60.5%; Pred. No. 5,1e-08;
Matches 92; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1045 CACAGATTGGTTTTCGGAGGCTTGAATTACCAAGTTGAGCACCATTGTTGGCCGACCT 1104
DB 456 CATGATTGGTCTTTGGTGATTACAGTTTCAGCTTGAGCATCATTTGTTCCCTCGCTT 397
QY 1105 CCCTCGCCCAACCTGACAGCGGTAGTACCAGGTGGAACAGCTGTGCCAGACACAA 1164
DB 396 ACCTGTTGGCATCTCGGAAAGTTTCTCCGGTGGTTCAGAGCTTTCGAAGAAGCATAA 337
QY 1165 CTTGCCGTATCGGAACCCGCTGCCCCCATGAAG 1196
DB 336 TCTCCGTATAGGAGTATGTCGTGTTGAAG 305
```

## RESULT 3

```
US-09-770-149-494/c
; Sequence 494, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Grlach, Jn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-494
```

```
Query Match 4.4%; Score 56; DB 10; Length 657;
Best Local Similarity 60.5%; Pred. No. 6.3e-08;
Matches 92; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1045 CACAGATTGGTTTTCGGAGGCTTGAATTACCAAGTTGAGCACCATTGTTGGCCGACCT 1104
DB 413 CATGATTGGTCTTTGGTGATTACAGTTTCAGCTTGAGCATCATTTGTTCCCTCGCTT 354
QY 1105 CCCTCGCCCAACCTGACAGCGGTAGTACCAGGTGGAACAGCTGTGCCAGACACAA 1164
DB 353 ACCTGTTGCCATCTCCGAAAGTTTCTCCGGTGGTTCAGAGCTTTCGAAGAAGCATAA 294
```



Query Match		4.0%;	Score 51;	DB 9;	Length 1474;	
Best Local Similarity		46.7%;	Pred. No. 5.1e-06;			
Matches 205;		Conservative	0;	Mismatches 225;	Indels	9; Gaps 1;
QY	791	CAGTATAAGAGGAGCCATTGGCCCTCGCCCTGACCTGGACCTTGAAGGCCCTGTTCAC	850			
DB	396	CATAAGAACTGGGTGACCTGGCCCTGGCGCTGAGTACTACATCCGGTTCATCACC	455			
QY	851	TTATTCTTTATGCCAGCATCTCTACATCGCTGTGGTGTTCGTTTCGGAGCTGGT	910			
DB	456	TACATCCCTTTCTACGGCATCTCGGGAGCCCTCTTTTCTCCTCACTTCACTCAGGTTCC	515			
QY	911	GGCGGCTTGGCATTCGGATCGGTGTTTCATGAAACCACTACCCACTGAGAGATCGGG	970			
DB	516	GAGAGCACTGGTGTGTGGGTCACACAGATGAATACATCTGTCATGAGATTTGACCA	575			
QY	971	GACCCAGTCTGGGATGGCCATGCTCGGTGGCCAGATCCATGAGACCATGAACATT	1030			
DB	576	GA-----GSCCTACCTGACTGTTTCAGTAGCCAGCTGACGCCACCTGCAACG	626			
QY	1031	CGCGAGGATTTATACAGATTCGTTTCGGAGGCTTGAATTTACCAAGTTGAGCACC	1090			
DB	627	GAGCAGTCTCTTCAACGACTGTTTCAGTGGACACTTAACCTCCAGATTTGACAC	686			
QY	1091	TTGTGGCGGACCTCTCCGCAACCTGACAGCGTTAGCTTACAGGTGGAACAGCTG	1150			
DB	687	CTCTTCCCAACCTGCGCGGCAACCTTACACAAGATCGCCCGCTGGTGAAGTCTCTA	746			
QY	1151	TGCGAGAGCACAACCTGCGGTATCGGAACCCGCTGCCCATGAAGGTTGGTCACTCTG	1210			
DB	747	TGTGCCAGCATGGCATTTGATACCAAGAGAGCCGCTACTGAGGCCCTGCTGGACATC	806			
QY	1211	CTCGGCTATCTGCGGTGT 1229				
DB	807	ATCAGGTCCTGAAGAAGT 825				
RESULT 7						
US-10-191-513A-6						
; Sequence 6, Application US/10191513A						
; Publication No. US20030104596A1						
; GENERAL INFORMATION:						
; APPLICANT: Abbott Laboratories						
; APPLICANT: Mukerji, Pardip						
; APPLICANT: Leonard, Amanda E.						
; APPLICANT: Huang, Yung-Sheng						
; APPLICANT: Tapas, Das						
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF						
; FILE REFERENCE: 6295.US.D3						
; CURRENT APPLICATION NUMBER: US/10/191,513A						
; CURRENT FILING DATE: 2002-09-25						
; PRIOR FILING DATE: 1999-01-08						
; PRIOR FILING DATE: 1999-01-08						
; PRIOR FILING DATE: 1998-04-10						
; PRIOR FILING DATE: 1997-04-11						
; NUMBER OF SEQ ID NOS: 54						
; SOFTWARE: FastSeq for Windows Version 4.0						
; SEQ ID NO 6						
; LENGTH: 1686						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-10-191-513A-6						
Query Match		4.0%;	Score 51;	DB 9;	Length 1686;	
Best Local Similarity		46.7%;	Pred. No. 5.6e-06;			
Matches 205;		Conservative	0;	Mismatches 225;	Indels	9; Gaps 1;
QY	791	CAGTATAAGAGGAGCCATTGGCCCTCGCCCTGACCTGGACCTTGAAGGCCCTGTTCAC	850			
DB	261	CATAAGAACTGGGTGACCTGGCCCTGGCGCTGAGTACTACATCCGGTTCATCACC	320			

QY	851	TTATTCTTTATGCCAGCATCTCTACATCGCTGTGGTGTTCGTTTCGGAGCTGGT	910			
DB	321	TACATCCCTTTCTACGGCATCTCGGGAGCCCTCTTTTCTCACTTCACTCAGGTTCTG	380			
QY	911	GGCGGCTTGGCATTCGGATCGGTGTTTCATGAACCACTACCCACTGGAGAAGATCGG	970			
DB	381	GAGAGCACTGGTGTGTGGTTCACACAGATGAATACATCTGTCATCGAGATTGACCA	440			
QY	971	GACCCAGTCTGGGATGGCCATGATTCCTCGGTGGCCAGATCCATGAGACCATGAAC	1030			
DB	441	GA-----GSCCTACCTGACTGTTTCAGTAGCCAGCTGACAGCCACCTGCAACG	491			
QY	1031	CGCGAGGATTTATACAGATTCGTTTCGGAGGCTTGAATTTACCAAGTTGAGCACC	1090			
DB	492	GAGCAGTCTCTTCAACGACTGTTTCAGTGGACACTTAACCTCCAGATTTGAGCACC	551			
QY	1091	TTGTGGCGGACCTCTCCGCAACCTGACAGCGTTAGCTTACCAAGTGGAAACAGCTG	1150			
DB	552	CTCTTCCCAACCTGCGCGGCAACCTTACACAAGATCGCCCGCTGGTGAAGTCTCTA	611			
QY	1151	TGCGAGAGCACAACCTGCGGTATCGGAACCCGCTGCCCATGAAGGTTGGTCACTCTG	1210			
DB	612	TGTGCCAAGCATGGCATTTGAATACCAAGAGAGCCGCTACTGAGGCCCTGCTGGACATC	671			
QY	1211	CTCGGCTATCTGCGGTGT 1229				
DB	672	ATCAGGTCCTGAAGAAGT 690				
RESULT 8						
US-10-191-513A-7						
; Sequence 7, Application US/10191513A						
; Publication No. US20030104596A1						
; GENERAL INFORMATION:						
; APPLICANT: Abbott Laboratories						
; APPLICANT: Mukerji, Pardip						
; APPLICANT: Leonard, Amanda E.						
; APPLICANT: Huang, Yung-Sheng						
; APPLICANT: Tapas, Das						
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF						
; FILE REFERENCE: 6295.US.D3						
; CURRENT APPLICATION NUMBER: US/10/191,513A						
; CURRENT FILING DATE: 2002-09-25						
; PRIOR FILING DATE: 1999-01-08						
; PRIOR FILING DATE: 1999-01-08						
; PRIOR FILING DATE: 1998-04-10						
; PRIOR FILING DATE: 1997-04-11						
; NUMBER OF SEQ ID NOS: 54						
; SOFTWARE: FastSeq for Windows Version 4.0						
; SEQ ID NO 7						
; LENGTH: 1843						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-10-191-513A-7						
Query Match		4.0%;	Score 51;	DB 9;	Length 1843;	
Best Local Similarity		46.7%;	Pred. No. 6e-06;			
Matches 205;		Conservative	0;	Mismatches 225;	Indels	9; Gaps 1;
QY	791	CAGTATAAGAGGAGCCATTGGCCCTCGCCCTGACCTGGACCTTGAAGGCCCTGTTCAC	850			
DB	418	CATAAGAACTGGGTGACCTGGCCCTGGCGCTGAGTACTACATCCGGTTCCTCATCACC	477			
QY	851	TTATTCTTTATGCCAGCATCTCTACATCGCTGTGGTGTTCGTTTCGGAGCTGGT	910			
DB	478	TACATCCCTTTCTACGGCATCTCGGGAGCCCTCTTTTCTCACTTCACTCAGGTTCTG	537			
QY	911	GGCGGCTTGGCATTCGGATCGGTGTTTCATGAACCACTACCCACTGGAGAAGATCGG	970			
DB	538	GAGAGCACTGGTGTGTGGTTCACACAGATGAATACATCTGTCATCGTACGATTGACCA	597			

QY 971 GACCCAGTCTGGGATGCCATGATCTCGTTGGCCAGATCCATGAGACCATTGAACATT 1030  
DB 598 GA-----GCGCTACCGTGACTGGTTCAAGTAGCCAGCTGACAGCCACCTGCAAGTG 648  
QY 1031 CGCGAGGAGTATACAGATTGGTTTTCGGAGGCTTGAATTAACAGATTGAGCACCAT 1090  
DB 649 GAGCAGTCTCTTCAACGACTGGTTCAAGTGACACTTAACATCCAGATTGAGCACCAC 708  
QY 1091 TTGTGGCCGACCTCCCTCGCCNACAACTGACAGCGGTAGCTPACAGGTGGAGACGCTG 1150  
DB 709 CTCCTTCCCACTGCGCCGACAACTTACACAAGATGCCCGCTGGTGAAGTCTCTA 768  
QY 1151 TGCCAGAGCAACACTGCGGTATCGGAACCCGCTGCCCATGAAGGTTGGTCATCCTG 1210  
DB 769 TGTGCCAACATGGCATTTGAATCCAGGAGACCGCTACTGAGGCCCTGCTGGACATC 828  
QY 1211 CTGCGCTATCTGCGGTGT 1229  
DB 829 ATCAGGTCCCTGAAGAAGT 847

## RESULT 9

US-10-191-513A-8  
; Sequence 8, Application US/10191513A  
; Publication No. US20030104596A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pardeep  
; APPLICANT: Leonard, Amanda E.  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Tapas, Dag  
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
; FILE REFERENCE: 6295.US.D3  
; CURRENT APPLICATION NUMBER: US/10/191,513A  
; PRIOR FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US 09/227,613  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/07422  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: US 08/833,610  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2257  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-191-513A-8

Query Match 4.0%; Score 51; DB 9; Length 2257;  
Best Local Similarity 46.7%; Pred. No. 6.8e-06;  
Matches 205; Conservative 0; Mismatches 225; Indels 9; Gaps 1;  
QY 791 CAGTATAGAGGAGGCCATGCGCTCGCCCTGCACTGGACCTTGAGGCCCTGTCCAC 850  
DB 832 CATAGAACTGGTGGACTGCGCTGGCCCTGAGCTACTATACATCCGTTCTTCATCAC 891  
QY 851 TTATCTTTATGCCAGCATCTCATCGCTGTTGGTCTTTTCTGTTTCGGAGCTGGTT 910  
DB 892 TACATCCCTTTCTACGGCATCTCGGAGCCCTCTTTCTCACTTCATCAGGTTCTG 951  
QY 911 GCGGCTTCGGCATTCGTGTGTTCAATGAACCACTACCCATGGAGAGATCGGG 970  
DB 952 GAGAGCCACTGTTGTGTGGTTCACACAGATGAATACATCGTCATGGAGATTGACCA 1011  
QY 971 GACCCAGTCTGGAGGCCATGGATTCTCGGTGGCCAGATCCATGAGACCATGAACATT 1030  
DB 1012 GA-----GGCCTACCGTGACTGGTTCAAGTAGCCAGCTGACAGCCACCTGCAACG 1062  
QY 1031 CGCGAGGAGTATACAGATTGGTTTTCGGAGGCTTGAATTAACAGATTGAGCACCAT 1090  
DB 1063 GAGCAGTCTTCTTCAACGACTGGTTCAAGTAGGACCACTTAACATCCAGATTGAGCACCAC 1122

QY 1091 TTGTGGCGGACCCCTCCCTCGCCCAACAACTGACAGCGGTAGCTACCAAGTGGAGACAGCTG 1150  
DB 1123 CTCCTTCCCACTGCGCCGACAACTTACACAAGATCGCCCGCTGGTGAAGTCTCTA 1182  
QY 1151 TGCCAGAGCAACACTGCGGTATCGGNACCCGCTGCCCATGAAGGTTGGTCATCCTG 1210  
DB 1183 TGTGCCAAGCATGGCATTTGAATCCAGGAGAACCGCTACTGAGGGCCCTGCTGGACATC 1242  
QY 1211 CTGCGCTATCTGCGGTGT 1229  
DB 1243 ATCAGGTCCCTGAAGAAGT 1261

## RESULT 10

US-10-156-761-1580  
; Sequence 1580, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1580  
; LENGTH: 1059  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1059)  
US-10-156-761-1580

Query Match 3.9%; Score 49.6; DB 9; Length 1059;  
Best Local Similarity 56.9%; Pred. No. 1.2e-05;  
Matches 91; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGATTCGCTGGCCAGATCCATGAGAC 1020  
DB 762 GGAATATGCGCGACCCCGACGCCACACGCTTGGGCCACCTGCGCGACAGAGTCTCACCTC 821  
QY 1021 CATGACATTCGCGAGGGGATTATCACAGATTGGTTTTTCGGAGGCTTGAATTACCAGAT 1080  
DB 822 GGCACAGTCTCGGGGGGTCGCTGACCGAGTGGTCTCGGGGACTCAACTACCAGAT 881  
QY 1081 TGAGCACCATTGTCGCGGACCTCCCTCGCCCAACCTG 1120  
DB 882 CGAGCACCATTGTTCCCGAGCATGCCCGCCCCCACTTG 921

## RESULT 11

US-10-156-761-1/c  
; Sequence 1, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRO

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      3.9%; Score 49.6; DB 9; Length 9025608;
Best Local Similarity 56.9%; Pred. No. 0.0045;
Matches 91; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGGATTCTCGGTGGCCAGATCCATGAGAC 1020
Db 1953719 GGAATGCCGACCCGACGACACACGCTTGGGCCACCTGGCGGACAGGTCTTCACCTC 1953660

Qy 1021 CATGAACATTCGGGAGGAGGATATACAGATTTGTTTCGGAGGCTTGAATTACACAGAT 1080
Db 1953659 CGCAACATTCGGGCGCGCTGCGCTGACCGACTGGTTCTCGGCGGACTCAACTACACAGAT 1953600

Qy 1081 TGACACACATTTGTGGCGGACCCCTCCCTCGGCACACACCTG 1120
Db 1953599 CGAGCACCATCTGTTCCCGAGCATGCCCGCCGCCACCTTG 1953560
```

```
RESULT 12
US-10-156-761-2285
; Sequence 2285, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2285
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1095)
US-10-156-761-2285

Query Match      3.8%; Score 48.6; DB 9; Length 1095;
Best Local Similarity 51.6%; Pred. No. 2.7e-05;
Matches 111; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 961 GAAGATCGGGGACCCAGTCTGGGATGGCCATGGATTCTCGGTGGCCAGATCCATGAGAC 1020
Db 762 GGAGTTCGGCGGACGCGAGGAGACCCCTGGACTGGCTGGAGCGGCGGAGTCTTCACCTC 821
```

```
Qy 1021 CATGAACATTCGGGAGGAGGATATACAGATTTGTTTCGGAGGCTTGAATTACACAGAT 1080
Db 822 CGGCAACATCCGCCCTCCCTGTTTCATCGACTTCTCTAGCGGCGCTCAACTACACAGT 881
Qy 1081 TGAGCACCATTTGTGGCGGACCCCTCCCTCGGCACACACCTGACAGCGGTAGCTACACAGT 1140
Db 882 CGAGCACCACTGTTCCCGGCGCATGCCAGAGAAACCTTGGCGCGCGCGGTGAACCTCAC 941
Qy 1141 GGAACAGCTGTGCCAGAGCACAACCTGCGCGTATC 1175
Db 942 CCGCGCTACTGCGCGAGCGCGGTGTGCGGTATC 976
```

```
RESULT 13
US-10-191-513A-37
; Sequence 37, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pardip
; APPLICANT: Leonard, Ananda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; FILE REFERENCE: 6295, US.D3
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: k = g or t/u at position 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37
```

```
Query Match      3.8%; Score 48.4; DB 9; Length 449;
Best Local Similarity 50.4%; Pred. No. 1.8e-05;
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 1006 CCAGATCCATGAGACCATTCGGGAGGAGGATTATCAGAGTTGGTTTTTCGGAGG 1085
Db 181 CCAGCTCCAGGCCACATGCAATGTCACAAAGTCTGCTTCAATGACTGGTTCAGTGACA 240
Qy 1066 CTTGAATTACAGATTGACACCAATTTGTGGCGGACCCCTCCCTCGGCACAACTGACAGC 1125
Db 241 CCTCAACTTCCAGATTGAGCACCATCTTTTCCACAGGATGCCCTCGACACAATTACCAAA 300
Qy 1126 GGTTAGCTACAGGTGGAAACAGCTGTGCGAGAGGACACACCTGCCGTATCGGAACCGCT 1185
Db 301 AGTGGTCCCTGGTGCAGTCTTGTGTGCCAGCATGGCATAGATACCAAGTCCCAAGCC 360
Qy 1186 GCCCATGAGGTTGGTCTCATCTGCTGCTATCTGGGGTGTTCGCCCGGAT 1239
Db 361 CCTGCTGTACGGCTTCGCCGACATCATCACTCACTAAAGAGTACAGGCGAGCT 414
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RESULT 14
US-10-191-513A-3
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Sequence 3, Application US/10191513A  
Publication No. US20030104596A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF.  
FILE REFERENCE: 6295.US.D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 655  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-191-513A-3

Query Match 3.8%; Score 48.4; DB 9; Length 655;  
Best Local Similarity 50.4%; Pred. No. 2.3e-05;  
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
QY 1006 CCAGATCCATGAGACCATGCGGAGGATTATCACAGATTGTTTCGGAGG 1065  
DB 175 CCAGCTCCAGGCCACATGTCACAACTGCTTCAATGACTGTTTCAGTGGACA 234  
QY 1066 CTTGAATTACAGATTGAGCACCATTGTCGCGACCTCCCTCGCCACAACCTGACAGC 1125  
DB 235 CCTCAACTCCAGATTGAGCACCATTCTTTCCACAGATGCTTCGACACAAATTACCACAA 294  
QY 1126 GGTAGTACCAGGTGAGCAGCTGTCGCGAGCTGTCGCGAGTATCGGAAACCCGCT 1185  
DB 295 AGTGCTCCCTGCTGTCAGTCTTGTGTCGCAAGCATGGCATAGATACCAAGTCCAAGCC 354  
QY 1186 GCGCATGAAGGTTGCTCATCTGCTGCGCTATCTGCGGGTTCGCCCGGAT 1239  
DB 355 CTTGCTGTCAGCTTCGCCGACATCATCCACTCACTAAAGGAGTCAAGGCGAGCT 408

RESULT 15  
US-10-191-513A-13  
Sequence 13, Application US/10191513A  
Publication No. US20030104596A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pardip  
APPLICANT: Leonard, Amanda E.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Tapas, Das  
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF  
FILE REFERENCE: 6295.US.D3  
CURRENT APPLICATION NUMBER: US/10/191,513A  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US 09/227,613  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: PCT/US98/07422  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: US 08/833,610  
PRIOR FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 864  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-191-513A-13

Query Match 3.8%; Score 48.4; DB 9; Length 864;  
Best Local Similarity 50.4%; Pred. No. 2.7e-05;  
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
QY 1006 CCAGATCCATGAGACCATGCGGAGGATTATCACAGATTGTTTCGGAGG 1065  
DB 603 CCAGCTCCAGGCCACATGCAATGTCACAACTGCTTCAATGACTGTTTCAGTGGACA 662  
QY 1066 CTTGAATTACAGATTGAGCACCATTGTCGCGACCTCCCTCGCCACAACCTGACAGC 1125  
DB 663 CCTCAACTTCAGATTGAGCACCATTCTTTCCACAGATGCTTCGACACAAATTACCACAA 722  
QY 1126 GGTAGTACCAGGTGGAACAGCTGTCGCGAGCTGTCGCGAGTATCGGAAACCCGCT 1185  
DB 723 AGTGCTCCCTGCTGTCAGTCTTGTGTCGCAAGCATGGCATAGATACCAAGTCCAAGCC 782  
QY 1186 GCGCATGAAGGTTGCTCATCTGCTGCGCTATCTGCGGGTTCGCCCGGAT 1239  
DB 783 CTTGCTGTCAGCTTCGCCGACATCATCCACTCACTAAAGGAGTCAAGGCGAGCT 836

Search completed: July 2, 2003, 19:28:30  
Job time : 242.694 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2003, 13:21:06 ; Search time 1973.08 Seconds  
(without alignments)  
10465.482 Million cell updates/sec

Title: US-09-857-583-3  
Perfect score: 1275  
Sequence: 1 atttttttcgaatgaagt.....gcgggggaagctctataagg 1275

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	74	5.8	689	13	BJ131677
C 2	74	5.8	748	13	BJ134106
C 3	73.2	5.7	762	13	BJ128407
C 4	72.8	5.7	705	13	BJ140668
5	72.6	5.7	696	13	BJ122807
6	72.4	5.7	563	13	BJ123410

7	72.4	5.7	594	13	BJ103098
8	72.4	5.7	623	13	BJ120260
C 9	72.4	5.7	627	13	BJ155885
C 10	72.4	5.7	689	9	AU209976
C 11	72.4	5.7	704	13	BJ137106
C 12	72.4	5.7	719	9	AU213658
C 13	72.4	5.7	720	9	AU210015
C 14	72.4	5.7	721	13	BJ151779
C 15	72.4	5.7	725	13	BJ152662
C 16	72.4	5.7	727	9	AU213941
C 17	72.4	5.7	731	13	BJ149141
C 18	72.4	5.7	742	13	BJ128934
C 19	72.4	5.7	743	13	BJ128630
C 20	72.4	5.7	746	13	BJ139067
C 21	72.4	5.7	750	13	BJ148511
C 22	72.4	5.7	756	13	BJ128883
C 23	72.4	5.7	761	13	BJ129368
C 24	72.4	5.7	763	13	BJ149952
C 25	72.4	5.7	773	13	BJ153638
C 26	72	5.6	650	9	AU215555
C 27	71.4	5.6	751	13	BJ146824
C 28	71	5.6	695	13	BJ128927
C 29	70.8	5.6	550	13	BJ135898
C 30	70.8	5.6	686	13	BJ138657
C 31	70.8	5.6	720	13	BJ130441
C 32	68.8	5.4	682	13	BJ130694
C 33	68.2	5.3	625	13	BJ136773
C 34	67.6	5.3	531	9	AU222176
C 35	67.6	5.3	534	13	BJ175250
C 36	67.6	5.3	576	13	BJ141357
C 37	67.6	5.3	605	9	AU217864
C 38	67.6	5.3	607	9	AU218049
C 39	67.6	5.3	612	13	BJ138911
C 40	67.6	5.3	627	13	BJ147665
C 41	67.6	5.3	639	13	BJ134940
C 42	67.6	5.3	639	13	BJ154428
C 43	67.6	5.3	655	13	BJ144819
C 44	67.6	5.3	671	13	BJ134613
C 45	66.6	5.2	526	10	BE445712

#### ALIGNMENTS

RESULT 1  
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LOCUS: BJ131677 689 bp mRNA linear EST 23-JAN-2002  
DEFINITION: BJ131677 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1057604 3', mRNA sequence.  
ACCESSION: BJ131677  
VERSION: BJ131677.1 GI:18291834  
KEYWORDS: EST.  
SOURCE: Caenorhabditis elegans.  
ORGANISM: Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.  
REFERENCE: 1 (bases 1 to 689)  
AUTHORS: Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y., and Sugano, S.  
TITLE: A complementary view of the C. elegans genome  
JOURNAL: Unpublished (2002)  
COMMENT: Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1..689  
/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"





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Db      367  ATAGATGTCAGCCCAATTCCTGAATTTTAAACAACCTTCGCCGCTCTTCAAATTTTGACCA 308
QY      1020 CCATGACATTCGGCAGGAGTATACAGATTGTTTTTCGGAGGCTTGAATTACCA 1079
Db      307  CACGCAACATGACTCCATTCATTCATGATGGCTTTGGGTGGAGTCAATATATCA 248
QY      1080 TTGAGCAGCATTTGTGGCGGAGCCTCCCTCGCCACAACCTGCAGCGGTAGTCAACAG 1139
Db      247  TCGAGCAGCAGCTGTTCACAACANTGCCAGCTTGCAATCTGAATGCTTGCATCAATATG 188
QY      1140 TGAACAGCTGTGCCAAGACACAACTGCCGTATC 1175
Db      187  TGAAGAATGGTGCAAGAAGATAATCTTCTCTTACC 152

RESULT 5
BJ122807
LOCUS      696 bp mRNA linear EST 23-JAN-2002
DEFINITION
Caenorhabditis elegans cDNA library, C. elegans L1 stage
VERSION    BJ122807
KEYWORDS   1 (bases 1 to 696)
SOURCE     Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
ORGANISM   Caenorhabditis elegans.
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 696)
AUTHORS    Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE      A complementary view of the C.elegans genome
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-I
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.

FEATURES             source
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     1..696
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     /strain="N2"
     /db_xref="taxon:6239"
     /clone="yk1292c05"
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     elegans L1 stage"
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     /tissue_type="whole animal"
     /dev_stage="L1"
     /note="The AD-wrmcDNA library was generated with poly(A)+
     RNA isolated from both hermaphrodite and male N2 worms of
     all larval stages, embryos, adults and dauers and the
     subsequent generation of cDNAs by poly(A) priming. The
     cDNAs were cloned into pPC86"

BASE COUNT    225 a 131 c 144 g 196 t
ORIGIN
Query Match      5.7%; Score 72.6; DB 13; Length 696;
Best Local Similarity 57.8%; Pred. No. 1.1e-10;
Matches 129; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY      382  GTATTTCATTTGGGCGAGTGTGCTTGGGATGCATATCAACAGATGGGCTGGCTTCTCA 441
Db      469  GTATATTACTTCTGCATGTTTATTAGCACTTGCATGCAACAATTCGGATGGTTAAACAC 528
QY      442  TGACATTTGCCACACAGACTTTCAGAACCGGAACCTGCAACAACCTCGTGGGACTGGT 501
Db      529  TGAGTTCTGCAATCAACAGCAACAAGAACACACCTTTTGAATGACACTATTTCTTTGTT 588
QY      502  ATTTGGCAATGTTCTGCAAGGTTTTTCCCGTGACATGTTGGAAGGACAGACAAATGCACA 561
Db      589  CTTTGGTATTTCTTACAGGATTTTCAAGAGATTTGGTGGAGGACAGCAATACACTCA 648

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QY      562  TCATTTCGGCAACCAATGTTCAAGGCGCACGACCTGATATTGAC 604
Db      649  TCAGCTGCCACAATGTAATGATCATGACGGTGATATCGAC 691

RESULT 6
BJ123410
LOCUS      563 bp mRNA linear EST 23-JAN-2002
DEFINITION
Caenorhabditis elegans cDNA clone yk1299e08 5', mRNA sequence.
VERSION    BJ123410
KEYWORDS   1 (bases 1 to 563)
SOURCE     EST.
            BJT123410.1 GI:18283549
            Caenorhabditis elegans.
            Caenorhabditis elegans.
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 563)
AUTHORS    Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE      A complementary view of the C.elegans genome
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-I
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.

FEATURES             source
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     /strain="N2"
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     /clone="yk1299e08"
     /clone_lib="unpublished oligo-capped cDNA library, C.
     elegans L1 stage"
     /sex="hermaphrodite"
     /tissue_type="whole animal"
     /dev_stage="L1"
     /note="The AD-wrmcDNA library was generated with poly(A)+
     RNA isolated from both hermaphrodite and male N2 worms of
     all larval stages, embryos, adults and dauers and the
     subsequent generation of cDNAs by poly(A) priming. The
     cDNAs were cloned into pPC86"

BASE COUNT    166 a 110 c 108 g 178 t
ORIGIN
Query Match      5.7%; Score 72.4; DB 13; Length 563;
Best Local Similarity 56.2%; Pred. No. 1.1e-10;
Matches 136; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY      382  GTATTTCATTTGGGCGAGTGTGCTTGGGATGCATATCAACAGATGGGCTGGCTTCTCA 441
Db      87  GTATATTACTTCTGCATGTTTATTAGCACTTGCATGCAACAATTCGGATGGTTAAACACA 146
QY      442  TGACATTTGCCACACAGACTTTCAGAACCGGAACCTGGAACACCTCGTGGGACTGGT 501
Db      147  TGAGTTCTGCGCATCAACAGCCCAACAAGAACAGACCTTTGAATGATATATTTCTTTGTT 206
QY      502  ATTTGGCAATGGTCTGCAAGGTTTTTCCGTCACATGTTGGAAGGACAGACACAATGCACA 561
Db      207  CTTTGGTAAATTTCTTACAAGGATTTTCAAGAGATTTGGTGGAGGACAGACATAACACTCA 266
QY      562  TCATTTCGGCAACCAATGTTCAAGGCGCACGACCTGATATTGACACACCTCCGCCCTTACC 621
Db      267  TCAGCTGCCACAATGTAATGATCATGACGGTGATATCGACTTGGCACCACCTTTTCGC 326
QY      622  CT 623
Db      327  AT 328

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## RESULT 7

BJ103098

## LOCUS

BJ103098

## DEFINITION

BJ103098

## ACCESSION

BJ103098

## VERSION

BJ103098

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans.

## ORGANISM

Caenorhabditis elegans.

## REFERENCE

1 (bases 1 to 594)

## AUTHORS

Kohara,Y., Shin-I,T., Thierri-Mieg,J., Thierri-Mieg,D., Suzuki,Y.

## TITLE

A complementary view of the C.elegans genome

## JOURNAL

Unpublished (2002)

## COMMENT

Contact: Tadasi Shin-I

## FEATURES

source

1..594

/organism="Caenorhabditis elegans"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1046b12"

/clone\_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/note="The AD-wrmcDNA library was generated with poly(A)+

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT 190 a 110 c 108 g 186 t

ORIGIN

Query Match 5.7%; Score 72.4; DB 13; Length 594;

Best Local Similarity 56.2%; Pred. No. 1.2e-10;

Matches 136; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 382 GTATTTCATTTGGGCGAGTGTCTTGGGATGCACATCAACAGATGGCTGCTTCTCA 441

DB 209 GTATATTACTTCTGCATGTTTATTAGCATTGGATGCAACAATTCGGATGGTTAACACA 268

QY 442 TGACATTTGCCACACAGACTTTCAAGAACCGGAACCTGCGTGGGACTGGT 501

DB 269 TGAGTTCTGCCATCAACAGCAACAAGACAGACCTTTCAATGATATCTATTCTTTGTT 328

QY 502 ATTTGGCAATGGTCTGAAGTTTTTCCGTCATGTTGGAAGGACAGACATGACACA 561

DB 329 CTTTGGTAAATTTCTTACAAAGGATTTTCAAGAGATTTGTTGGAAGGACAAAGCATACACTCA 388

QY 562 TCATTGGGCAACCAATGTTCAAGGGCAGCAGCTTATTTGACACACCTCCGCCCTTAGC 621

DB 389 TCACGCTGCCAACAATGTAATGATCATGCGGTGATATCGACTTGGCACCACCTTTTCGC 448

QY 622 CT 623

DB 449 AT 450

## RESULT 8

BJ120260

## LOCUS

BJ120260

## DEFINITION

BJ120260

## ACCESSION

BJ120260

## VERSION

BJ120260

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans.

## ACCESSION

BJ120260

## VERSION

BJ120260

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans.

## ORGANISM

Caenorhabditis elegans.

## REFERENCE

1 (bases 1 to 623)

## AUTHORS

Kohara,Y., Shin-I,T., Thierri-Mieg,J., Thierri-Mieg,D., Suzuki,Y.

## TITLE

A complementary view of the C.elegans genome

## JOURNAL

Unpublished (2002)

## COMMENT

Contact: Tadasi Shin-I

## FEATURES

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1..623

/organism="Caenorhabditis elegans"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1253h09"

/clone\_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/note="The AD-wrmcDNA library was generated with poly(A)+

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT 207 a 112 c 117 g 187 t

ORIGIN

Query Match 5.7%; Score 72.4; DB 13; Length 623;

Best Local Similarity 56.2%; Pred. No. 1.2e-10;

Matches 136; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 382 GTATTTCATTTGGGCGAGTGTCTTGGGATGCACATCAACAGATGGCTGCTTCTCA 441

DB 374 GTATATTACTTCTGCATGTTTATTAGCATTGGATGCAACAATTCGGATGGTTAACACA 433

QY 442 TGACATTTGCCACACAGACTTTCAAGAACCGGAACCTGCGTGGGACTGGT 501

DB 434 TGAGTTCTGCCATCAACAGCAACAAGACAGACCTTTGAATGATATCTATTCTTTGTT 493

QY 502 ATTTGGCAATGGTCTGCAAGGTTTTTCGCTGACATGTTGGAAGGACAGACAACTGACACA 561

DB 494 CTTTGGTAAATTTCTTACAAGGATTTTCAAGAGATTTGTTGGAAGGACAGCACTCA 553

QY 562 TCATTGGCAACCAATGTTTCAAGGCGACGACCTGATATGACACCTCCGCCCTTAGC 621

DB 554 TCACGCTGCCAACAATGTAATGATCATGAGGTGATATCGACTTGGCACCACCTTTTCGC 613

QY 622 CT 623

DB 614 AT 615

## RESULT 9

BJ155885/C

## LOCUS

BJ155885

## DEFINITION

BJ155885

## ACCESSION

BJ155885

## VERSION

BJ155885

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans.

Caenorhabditis elegans cDNA clone yk1253h09 5', mRNA sequence.

BJ120260

BJ120260.1 GI:18280388

EST.

Caenorhabditis elegans.

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 623)

Kohara,Y., Shin-I,T., Thierri-Mieg,J., Thierri-Mieg,D., Suzuki,Y.

and Sugano,S.

A complementary view of the C.elegans genome

Unpublished (2002)

Contact: Tadasi Shin-I

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1..623

/organism="Caenorhabditis elegans"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1253h09"

/clone\_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/note="The AD-wrmcDNA library was generated with poly(A)+

RNA isolated from both hermaphrodite and male N2 worms of

all larval stages, embryos, adults and dauers and the

subsequent generation of cDNAs by poly(A) priming. The

cDNAs were cloned into pPC86"

BASE COUNT 207 a 112 c 117 g 187 t

ORIGIN

Query Match 5.7%; Score 72.4; DB 13; Length 623;

Best Local Similarity 56.2%; Pred. No. 1.2e-10;

Matches 136; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 382 GTATTTCATTTGGGCGAGTGTCTTGGGATGCACATCAACAGATGGCTGCTTCTCA 441

DB 374 GTATATTACTTCTGCATGTTTATTAGCATTGGATGCAACAATTCGGATGGTTAACACA 433

QY 442 TGACATTTGCCACACAGACTTTCAAGAACCGGAACCTGCGTGGGACTGGT 501

DB 434 TGAGTTCTGCCATCAACAGCAACAAGACAGACCTTTGAATGATATCTATTCTTTGTT 493

QY 502 ATTTGGCAATGGTCTGCAAGGTTTTTCGCTGACATGTTGGAAGGACAGACAACTGACACA 561

DB 494 CTTTGGTAAATTTCTTACAAGGATTTTCAAGAGATTTGTTGGAAGGACAGCACTCA 553

QY 562 TCATTGGCAACCAATGTTTCAAGGCGACGACCTGATATGACACCTCCGCCCTTAGC 621

DB 554 TCACGCTGCCAACAATGTAATGATCATGAGGTGATATCGACTTGGCACCACCTTTTCGC 613

QY 622 CT 623

DB 614 AT 615

## RESULT 9

BJ155885/C

## LOCUS

BJ155885

## DEFINITION

BJ155885

## ACCESSION

BJ155885

## VERSION

BJ155885

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans.

Caenorhabditis elegans cDNA clone yk1347d06 3', mRNA sequence.

BJ155885

BJ155885.1 GI:18323870

EST.

Caenorhabditis elegans.

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ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS 1 (bases 1 to 627)
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@nig.ac.jp.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:6239"
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elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPCR86"
BASE COUNT 187 a 119 c 134 g 186 t 1 others
ORIGIN
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Best Local Similarity 47.7%; Pred. No. 1.2e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
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DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 592 CTCGAAGATGTACCATATCAACATCTCTATTTACCGCAATGTTTCAATGCTCCGTTTC 533
QY 722 ATTTGGTGTTCAGTGCCTGTTGACCGTCGCGATTTGAAGGACAGACATAACCAATTC 781
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 532 TCATGACGCTGTCAGTCAGTTCATGGGTATTTCAAGAGAAATCAATGGAGTCAAGGTC 473
QY 782 TATCGCTCTCAGTATAAGAGAGGCGCATTTGGCTCGCCCTGCACCTGGACCTTGAAGGCC 841
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QY 472 TATCAAGAAATGCATTTCTGGGAGCAAGCAACAATTTGGACATTTGGGCTT---GGGTA 416
QY 842 CTGTTCCACTTATTTATGCCCCAGCATCTCACATCGCTGTGTGTTGTTTTCGTTTCG 901
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 415 TTCTATCAATTTGTTCTTATTTACCAACATGCGGCTTCTGTTTATTTCAATTTTCA 356
QY 902 GAGCTGTGGCGCTTCGGCATTCGATCGATCGGTGTTTCATGAACCACTACCCACTCGAG 961
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 355 CAATGGGAGGAGGCTTTTGATGTCTCAGTACTTCAACCACTACTCTGTGTGAT 296
QY 962 AAGATCGGGACACGCTCTGGGATGGCCATGGATTTCTGTTGGCCAGATCCATGAGACC 1021
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 295 AAGTATCCAGCCAAATCTCGAATTTTAAACAATTCGCGCTCTTCAAAATTTTGACCACA 236
QY 1022 ATGAACATTCGGGAGGATTTACAGATTTGTTTTCGGAGGCTTGAATTTACCAATT 1081
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 235 CGCAACATGACTCCATCTCCATTTCAATTTGATTTGGCTTTGGGGTGGACTCAATTTACATC 176
QY 1082 GAGCAGCTTTGTGGCGGACCTCCCTCGCCGCAACCTGACAGCGGTAGCTACCAAGTG 1141
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 175 GAGCAGCCTTTGTTCCCAACAATGCCACGTTGGAATCTGAATGCTTGCATGAATATGTG 116
QY 1142 GAACAGCTGTGCCAGAGCAACAACCTGCCGCTATC 1175
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
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DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
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LOCUS AU209976 unpublished oligo-capped cDNA library, stage L1
DEFINITION Caenorhabditis elegans cDNA clone yk751c07 3', mRNA sequence.
ACCESSION AU209976
VERSION AU209976.1 GI:14845938
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS 1 (bases 1 to 689)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2001)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
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source Location/Qualifiers
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/organism="Caenorhabditis elegans"
/strain="N2"
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/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPCR86"
BASE COUNT 228 a 121 c 146 g 194 t
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Query Match 5.7%; Score 72.4; DB 9; Length 689;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
QY 662 CGCAAGCTCATTCAGTTCAGCAGTACTATTTCTTGTCATCTGTATCTTGTGCGGTTTC 721
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 687 CTCGAAGATGTACCATATCAACATCTCTATTTACCGCAATGCTTCCATGCTCCGTTTC 628
QY 722 ATTTGGTGTTCAGTGCCTGTTGACCGTCGCGATTTTGAAGGACAGAGATAACCAATTC 781
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 627 TCATGGACTGTGTCAGTTCATGGGTATTTCAAGAGAAATCAATGGAGTCAAGGTC 568
QY 782 TATCGCTCTCAGTATAAGAGAGGCGCATTTGGCTCGCCCTGCACCTGGACCTTGAAGGCC 841
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 567 TATCAAGAAATGCAATCTCTGGGAGCAAGCAACAATTTTGGACATTTGGGCTT---GGGTA 511
QY 842 CTGTTCCACTTATTTCTTATGCCCCAGCATCTCACATCGCTGTGTGTTTTCGTTTCG 901
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 510 TTCTATCAATTTGTTCTTATTTACCAACATGCGGCTTTCGTTTATTTCAATTTTCA 451
QY 902 GAGCTGTGGCGGCTTCGGCATTCGCGATTCGATCGGTGTTTCATGAACCACTACCCACTGGAG 961
DB 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 450 CAATGGGAGGAGGCGCTTTTGATGCTCAGTACTTTCACCACTCAACTCTGTGTGAT 391
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QY 390 AAGTATCCAGCCAAATTTCTCGAATTTTAAACAATTCGCGGCTCTTCAAAATTTTGACCACA 331
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1022 ATGAACATTCGGCGAGGATATACAGATTGGTTTTCGGAGGCTTGAATTACCAGATT 1081
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Db    330 CGCACATGACTCCATCTCCATTGATGGCTTTGGGGTGGACTCAATATACAGATC 271
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy    1082 GAGCACCATTGTTGGCGGACCTCCCTCGCCACACACCTGACAGCGGTAGCTACCAGGTG 1141
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    270 GAGCACCATTGTTGCCCAACAATGCCAGTTCGAATCTGAATGCTTGCAATGAATATGTG 211
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Qy    1142 GAACAGCTGTGCCAGACACAACTGCGCGTATC 1175
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Db    210 AAAGATGGTGCAAGAGAATAATCTCTTACC 177
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
BJ137106/c
LOCUS
DEFINITION
  BJ137106 unpublished oligo-capped cDNA library, C. elegans L1 stage
  Caenorhabditis elegans cDNA clone yk1120e02 3', mRNA sequence.
ACCESSION
  BJ137106
VERSION
  BJ137106.1 GI:18297272
KEYWORDS
  EST.
SOURCE
  Caenorhabditis elegans.
  Caenorhabditis elegans.
  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
  1 (bases 1 to 704)
REFERENCE
  Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
  and Sugano,S.
  A complementary view of the C.elegans genome
  Unpublished (2002)
  Contact: Tadasu Shin-1
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshin@nig.ac.jp.
  Location/Qualifiers
    1. 704
      /organism="Caenorhabditis elegans"
      /strain="N2"
      /db_xref="taxon:6239"
      /clone="yk1120e02"
      /clone_lib="unpublished oligo-capped cDNA library, C.
      elegans L1 stage"
      /sex="hermaphrodite"
      /tissue_type="whole animal"
      /dev_stage="L1"
      /note="The AD-wrmcDNA library was generated with poly(A)+
      RNA isolated from both hermaphrodite and male N2 worms of
      all larval stages, embryos, adults and dauers and the
      subsequent generation of cDNAs by poly(A) priming. The
      cDNAs were cloned into pPC86"
BASE COUNT
  231 a 123 c 148 g 202 t
ORIGIN
  5.7%; Score 72.4; DB 13; Length 704;
  Best Local Similarity 47.7%; Pred. No. 1.3e-10;
  Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;

Qy    662 CGCAAGCTCATTCAGTTCACAGACTATTTCTGGTCATCTGTTGGTTCATCTGTTGGCGTTC 721
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    704 CTCGAAGATTGTACCATATACATCTCTATTATTCACCGCAATGCTTCCAAATGCTCGGTTTC 645
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Qy    722 ATTTGGTGTTCAGTGGTGTTCACCGTGGCGAGTTGAAGGACAGAGATAACCAATTC 781
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Db    644 TCATGGAGTGTCTAGTCAGTTCAATGGGTATTCAAAGAGAATAATCAATGGAGTACAAGTTC 585
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy    782 TATCGCTCTCAGTATAAGAGGAGGCCATTGGCTCGCCCTGCGACTGGAGCCTTGAAGGCC 841
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    584 TATCAAGAATAATGCAATCTCTGGGACCAAGCAACAATTTGTTGACATATGGGCTT---GGGTA 528
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy    842 CTGTTCCACTTATCTTTATATGCCAGCATCCTCATCTGCTGTGGTGTGTTTTCGTTTCG 901
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527 TTCTATCAATTTGTTCTTATATACCAACATGGCCACTTCGGGTGCTTATTTCAATTATTTCA 468
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Qy    902 GAGCTGGTTGGGGGTTTCGGCATTTGCGATCGTGGTGTTCATGAACCACTACCACCTGAG 961
      || | |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    467 CAATGGGAGGAGGCCCTTTTGGTTCAGTACAGTACACCTTTCAACCACTAATCTGTTGAT 408
      || | |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy    962 AAGATCGGGGAGCCAGTCTGGGATGGCCATGGATTTCTCGTTCGGTTCGCCAGATCCATGAGACC 1021
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Db    407 AAGTATCCAGCCAATTTCTCGAATTTTAAACAACCTCGCCGCTCTTCAAATTTTGACCACA 348
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Qy    1022 ATGAACATTCGGCGAGGATATACAGATTGGTTTTCGGAGGCTTGAATTACCAGATT 1081
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    347 CGCACATGACTCCATCTCCATTGATGGCTTTGGGGTGGACTCAATATACAGATC 288
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy    1082 GAGCACCATTGTTGGCGGACCTCCCTCGCCACACACCTGACAGCGGTAGCTACCAGGTG 1141
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    287 GAGCACCATTGTTGCCAACAATGCCAGCTTGAATCTGAATCTTGCATGAATATGTG 228
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Qy    1142 GAACAGCTGTGCCAGACACAACTGCGCGTATC 1175
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AU213658/c
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DEFINITION
  AU213658 unpublished oligo-capped cDNA library, stage L1
  Caenorhabditis elegans cDNA clone yk803b11 3', mRNA sequence.
ACCESSION
  AU213658
VERSION
  AU213658.1 GI:14851815
KEYWORDS
  EST.
SOURCE
  Caenorhabditis elegans.
  Caenorhabditis elegans.
  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
  1 (bases 1 to 719)
REFERENCE
  Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
  and Sugano,S.
  A complementary view of the C.elegans genome
  Unpublished (2001)
  Contact: Yuji Kohara
  Genome Biology Lab.
  National Institute of Genetics
  Yata 1111, Mishima, Shizuoka 411, Japan
  Tel: 81-559-81-6854
  Fax: 81-559-81-6855
  Email: ykohara@lab.nig.ac.jp.
  Location/Qualifiers
    1. 719
      /organism="Caenorhabditis elegans"
      /strain="N2"
      /db_xref="taxon:6239"
      /clone="yk803b11"
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      L1"
      /sex="Hermaphrodite"
      /tissue_type="whole animal"
      /dev_stage="L1"
      /note="The AD-wrmcDNA library was generated with poly(A)+
      RNA isolated from both hermaphrodite and male N2 worms of
      all larval stages, embryos, adults and dauers and the
      subsequent generation of cDNAs by poly(A) priming. The
      cDNAs were cloned into pPC86"
BASE COUNT
  228 a 129 c 152 g 206 t
ORIGIN
  5.7%; Score 72.4; DB 9; Length 719;
  Best Local Similarity 47.7%; Pred. No. 1.3e-10;
  Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;

Qy    662 CGCAAGCTCATTCAGTTCACAGACTATTTCTGGTTCATCTGTTGGTTCATCTGTTGGCGTTC 721
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686 CTCAAGATGTACCATATCAACATCTCTATTTCACGCAATGCTTCCAATGCTCCGTTTC 627
QY 722 ATTTGGTGTTCACAGTCTGTGGACCGTGGCGAGTTTTCAGGACAGAGATACCAATTC 781
Db 626 TCATGGACTGGTCAGTCAGTCTCAATGGGTATTCAAGAGAAATCAGATGGAGTACAAGGTC 567
QY 782 TATCGCTCTCAGTATAGAAGAGGAGGCAATTTGGCCTCGCCCTGCACCTGGACCTTGAAGGCC 841
Db 566 TATCAAGAAGATGCATCTCTGGGAGCAAGCAACAAATTTGTCACATTTGGGCTT--GGTA 510
QY 842 CTGTTCCACTTATCTTTATGCCCAGCATCTCAGATCGCTGTGGTGTGTTTTCGTTTCG 901
Db 509 TTCTATCAATTTCTTATTACCAATGCGCACTTCGGGTTGCTTATTTCATTTATTC 450
QY 902 GAGCTGGTGGGGCTTCGGCATGCGATGCTGGTCTTCATGAACCACTACCACTGGAG 961
Db 449 CAAATGGGAGGAGGCTTTTGATTTGCTCAGTAGTCACCTTTCANCCATTAACCTGTGTAT 390
QY 962 AAGATCGGGAGCCAGCTCTGGATGGCCATGATTCCTCGTGTGGCCAGATCCATGAGACC 1021
Db 389 AAGTATCCAGCAATTTCTCGAATTTTAAACAACCTTCGCGCTCTTCAAAATTTTGACCACA 330
QY 1022 ATGAACATTCGGGAGGAGTATATCAGATTTGTTTTCGGAGGCTTGAATTAACAGATT 1081
Db 329 CGCAACATGACTCCATCTCCATTCATTTGATTTGGCTTTGGGGTGGACTCAATATATCAGATC 270
QY 1082 GAGCACCATTGTGGCGGACCTTCCTCGCCACAACCTGACAGCGGTTAGCTACCAAGTG 1141
Db 269 GAGCACCATTGTTCACCAATATGCCCAGTTCGAATCTGAATCTTGCATGAATATATG 210
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Db 209 AAAGATGGTGCAAGAGATAATCTCTCTTACC 176

RESULT 13
AU210015/c
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AU210015 720 bp mRNA linear EST 17-JUL-2001
AU210015 unpublished oligo-capped cDNA library, stage L1
Caenorhabditis elegans cDNA clone yk751h06 3', mRNA sequence.
AU210015
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
1 (bases 1 to 720)
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2001)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykoha@lab.nig.ac.jp.
Location/Qualifiers
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pc86"
BASE COUNT 234 a 127 c 152 g 207 t
ORIGIN
Query Match 5.7%; Score 72.4; DB 9; Length 720;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
QY 662 CGCAAGCTCAATTCAGTTCACGACGACTACTATTCTTGGTCTCATCTGTATCTTGGTGGGTTTC 721
Db 687 CTCGAAGATTGTACCATATCAACATCTCTATTTCACGCAATGCTTCCAATGCTCCGTTTC 628
QY 722 ATTTGGTGTTCACAGTCTGTGGACCGTGGCGAGTTTTCAGGACAGAGATACCAATTC 781
Db 626 TCATGGACTGGTCAGTCAGTCTCAATGGGTATTCAAGAGAAATCAGATGGAGTACAAGGTC 568
QY 782 TATCGCTCTCAGTATAGAAGAGGAGGCAATTTGGCCTCGCCCTGCACCTGGACCTTGAAGGCC 841
Db 566 TATCAAGAAGATGCATCTCTGGGAGCAAGCAACAAATTTGTCACATTTGGGCTT--GGTA 511
QY 842 CTGTTCCACTTATCTTTATGCCCAGCATCTCAGATCGCTGTGGTGTGTTTTCGTTTCG 901
Db 510 TTCTATCAATTTCTTATTACCAATGCGCACTTCGGGTTGCTTATTTCATTTATTC 451
QY 902 GAGCTGGTGGGGCTTCGGCATGCGATGCTGGTCTTCATGAACCACTACCACTGGAG 961
Db 450 CAAATGGGAGGAGGCTTTTGATTTGCTCAGTAGTCACCTTTCACCACTAATCTGTGTAT 391
QY 962 AAGATCGGGAGGAGTATATCAGATTTGTTTTCGGAGGCTTGAATTAACAGATT 1081
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QY 1022 ATGAACATTCGGGAGGAGTATATCAGATTTGTTTTCGGAGGCTTGAATTAACAGATT 1081
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QY 1082 GAGCACCATTGTGGCGGACCTTCCTCGCCACAACCTGACAGCGGTTAGCTACCAAGTG 1141
Db 270 GAGCACCATTGTTCACCAATATGCCCAGTTCGAATCTGAATCTTGCATGAATATATG 211
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BJ151779 721 bp mRNA linear EST 24-JAN-2002
BJ151779 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1299e08 3', mRNA sequence.
BJ151779
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
1 (bases 1 to 721)
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsini@genes.nig.ac.jp.
Location/Qualifiers
1. .721
/organism="Caenorhabditis elegans"
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/strain="N2"
/db.xref="taxon:6239"
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elegans L1 stage"
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/tissue_type="whole animal"
/dev_stage="L1"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT      236 a 128 c 149 g 207 t      1 others
ORIGIN
Query Match      5.7%; Score 72.4; DB 13; Length 721;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 245; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
Qy 662 CGAAGCTCATTCAGTCCAGCAGTACTATTTCTGGTCACTCTATCTGTTGGGTTTC 721
Db 685 CTCAAGATTGACCATATCAATCTCTATTTACCGCAATGCTTCCAATGCTCCGTTTC 626
Qy 722 ATTTGGTGTTCAGTCGGTGTTCACCGTCGGCAGTTTGAAGGACAGAGATAACCAATTC 781
Db 625 TCATGGACTGGTCAGTCAATGGGTATTTCAAGAGAAATCAATGGAGTACAAGGTC 566
Qy 782 TATCGCTCTCAGTATAGAAGGCGCATTTGGCTCGCCCTGCACCTGGACCTTGAAGGCC 841
Db 565 TATCAAGAAATGCATTTCTGGAGCAAGCAACAATTTGTGGACATTTGGGCTT---GGTA 509
Qy 842 CTGTTCCACTATTTCTTTATGCCAGCATCTCATCGCTGTGGTGTGTTTTCGTTTCG 901
Db 508 TTCTATCAATTTGTTTATTACCAACATGGCCACTTCGGGTGTGTTTATTCATTATTTCA 449
Qy 902 GAGCTGTTGGCGCTTCGGCATTCGATCGTGTGTTTCATGAACCACTACCCACTGGAG 961
Db 448 CAATGGAGGAGGCGCTTTTGATTGTCAGTACTACTTTCAACCAATCACTCTGTGTAT 389
Qy 962 AAGATCGGGGACCCAGTCTGGGATGGCCATGGATTTCTGGTTGGCCAGATCCATGAGACC 1021
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Qy 1022 ATGAACATTCGGGAGGGATATACAGATGTTGTTTTCGGAGCGTTGAATACCAATTC 1081
Db 328 CGCAACATGACTCCATCTCCATTCATTTGATTTGGGCTTTGGGCTGACTCAATATCAGATC 269
Qy 1082 GAGCACCATTGTGGCGGACCCCTCCCTCGCCACACCTGACAGCGGTTAGCTACCGGTG 1141
Db 268 GAGCACCATTGTTCACCAAAATGCCAGTTGCAATCTGAATGCTTCATGAATATATGTG 209
Qy 1142 GAACAGCTGTGCCAGAACCAACCTGCCGCTATC 1175
Db 208 AAAGAATGGTGCAAGAGAAATATCTTCCTTACC 175

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RESULT 15
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LOCUS      725 bp mRNA linear EST 24-JAN-2002
DEFINITION BJ152662 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1310b09 3', mRNA sequence.
ACCESSION BJ152662
VERSION    BJ152662.1 GI:18320647
KEYWORDS  EST.
SOURCE    Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Rukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS : Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 725)
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,I.Y.
and Sugano,S.
A complementary view of the C.elegans genome.
TITLE

```

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JOURNAL      Unpublished (2002)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshin@genes.nig.ac.jp.
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                /tissue_type="whole animal"
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                /note="The AD-wrmcDNA library was generated with poly(A)+
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                cDNAs were cloned into pPC86"
BASE COUNT    235 a 131 c 149 g 210 t
ORIGIN

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Best Local Similarity 47.7%; Pred. No. 1.3e-10;
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